

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 05:21:02 ; Search time 5453 Seconds
(without alignments)
11058.577 Million cell updates/sec

Title: US-09-857-346A-2

Perfect score: 943

Sequence: 1 cgagaaagagaaaaaa.....tgagaaaaaa..... 943

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_env.*
2: gb_pat.*
3: gb_ph.*
4: gb_pl.*
5: gb_pr.*
6: gb_to.*
7: gb_sts.*
8: gb_sy.*
9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_htg.*
13: gb_in.*
14: gb_om.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	943	100.0	943	2	BD272883
2	943	100.0	943	4	AF116527
3	792	84.0	806	4	AY964095
4	787.2	83.5	806	4	AY964094
5	784.4	83.2	797	2	BD268759
6	784.4	83.2	797	2	AR476092
7	784.4	83.2	801	4	AF537203
8	770.8	81.7	774	4	AY850001
9	686	72.7	842	4	AY850000
10	680	72.1	732	4	AY850002
11	593.8	63.0	651	4	DQ167446
12	591	62.7	591	4	AY964092
13	591	62.7	591	4	AY964097
14	591	62.7	599	4	AY964093
15	587.4	62.3	651	4	DQ167444
16	587	62.2	591	4	AY964090
17	543	57.6	591	4	DQ167447
18	538.4	57.1	868	2	BD272888

19	528	56.0	845	2	BD272892	BD272892	Control o
20	528	56.0	845	4	AY036888	AY036888	Brassica
21	527	55.9	891	2	BD272894	BD272894	Control o
22	523.4	55.5	565	4	AY964091	AY964091	Arabidops
23	494.8	52.5	969	2	BD272887	BD272887	Control o
24	491.8	52.5	969	4	AY036890	AY036890	Brassica
25	491.8	52.2	851	4	AY364013	AY364013	Brassica
26	490.8	52.0	825	2	BD272893	BD272893	Control o
27	488.4	51.8	666	4	AY306123	AY306123	Brassica
28	484	51.3	990	2	BD272890	BD272890	Control o
29	480.4	50.9	822	4	AY308848	AY308848	Brassica
30	477.4	50.6	908	2	BD272885	BD272885	Control o
31	477.4	50.6	908	4	AY036891	AY036891	Brassica
32	471.4	50.0	780	2	BD272891	BD272891	Control o
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34	468.4	49.7	847	2	BD272886	BD272886	Control o
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44	448.6	47.6	867	2	AR476096	AR476096	Sequence
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ALIGNMENTS

RESULT 1
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LOCUS BD272883 943 bp DNA linear PAT 17-JUL-2003
DEFINITION Control of flowering.
ACCESSION BD272883
VERSION BD272883.1 GI:33082651
KEYWORDS JP 2002532069-A/2.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 943)
AUTHORS Burn,J.E., Peacock,W.J., Dennis,E.S., Sheldon,C.C., Perez,P., Helliwell,C.A. and Rouse,D.T.
TITLE Control of flowering
JOURNAL Patent: JP 2002532069-A 2 02-OCT-2002;
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION,
PASCUAL PEREZ
COMMENT OS Arabidopsis thaliana (thale cress)
PN JP 2002532069-A/2
PD 02-OCT-2002
PF 02-DEC-1999 JP 2000585411
PR 03-DEC-1998 AU PP 7469,22-JAN-1999 US 60/116928 PI
JOANNE ELIZABETH BURN, WILLIAM JAMES PEACOCK, ELIZABETH PI
SALISBURY DENNIS,
PI CANDICE CLAIRE SHELTON, PASCUAL PEREZ, CHRISTOPHER ANDREW PI
HELLIWELL,
PI DEAN THOMAS ROUSE
PC C12N15/09,A01H5/00,C07K14/415,C07K16/16,C12N5/10,C12Q1/68, PC
G01N33/53,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC Control
of flowering
FH Key Location/Qualifiers
FT source 1..943
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Location/Qualifiers
1..943
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/mol_type="genomic DNA"

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Qy	361	GTCAAAGCTCTGAATCTGGTTTCACTATGAGCTACTTGAACCTTGTGGATAGCAAGCT	420
Db	361	GTCAAAGCTCTGAATCTGGTTTCACTATGAGCTACTTGAACCTTGTGGATAGCAAGCT	420
Qy	421	TGTGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTGTGTTCACTCGAGAACACCT	480
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Qy	481	TGAGATCGCCCTCTCGCTGACTAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	540
Db	481	TGAGATCGCCCTCTCGCTGACTAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	540
Qy	541	GAATCTTAAAGAAAGAGAGAAATGCTGAAAGAGAGAAACAGGTTTGGCTAGCCAGAT	600
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Qy	901	ATGAACCTTTGTATCTTATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	943
Db	901	ATGAACCTTTGTATCTTATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	943

AF116527
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Arabidopsis thaliana 943 bp mRNA
Arabidopsis thaliana cultivar Columbia MADS box protein FLOWERING LOCUS F (FLF) mRNA, complete cds.
AF116527
AF116527.1 GI:4469407

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 943)
Sheldon, C.C., Burn, J.E., Perez, P.P., Metzger, J., Edwards, J.A., Peacock, W.J. and Dennis, E.S.
The FLF MADS box gene: a repressor of flowering in Arabidopsis regulated by vernalization and methylation
Plant Cell 11 (3), 445-458 (1999)
10072403

2 (bases 1 to 943)
Sheldon, C.C.
Direct Submission
Submitted (22-DEC-1998) Plant Industry, CSIRO, GPO Box 1600, Canberra, ACT 2600, Australia
Location/Qualifiers
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/mol_type="mRNA"
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ORIGIN

Query Match 100.0%; Score 943; DB 4; Length 943;
Best Local Similarity 100.0%; Pred. No. 5.9e-283;
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 CCAACCTGAGGATCAAAATTAGGCGCAAAAGCCCTCTCGAGAGAGCCATCGGAGAAA 120
Qy 121 AAAACTAGAAATCAAGCGAATTCAGAACAAAGTACCGACAGTCACTTCTCCAAACG 180
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Qy 241 TCCTCTCGTCTCGGCTCCGGCAAGCTCTACAGCTTCTCTCGGGCGATAACCTGGT 300
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Db	301	CAAGATCTCTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA	360
Qy	361	GTCAAAAGCTCTGAACACTATGGTTTCACACTATGAGTACTTGAACCTTGGATGAGCAAGCT	420
Db	361	GTCAAAAGCTCTGAACACTATGGTTTCACACTATGAGTACTTGAACCTTGGATGAGCAAGCT	420
Qy	421	TGTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCAACTGGAGGAACACT	480
Db	421	TGTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCAACTGGAGGAACACT	480
Qy	481	TGAGACTGCTCTCTCGGTGACTAGAGCCAAAGAACCGAAGCTCATGTTGAAAGCTTGTGGA	540
Db	481	TGAGACTGCTCTCTCGGTGACTAGAGCCAAAGAACCGAAGCTCATGTTGAAAGCTTGTGGA	540
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Qy	721	AAATCAAAATCCAAACATATATTAATTAAGAAAAAATAAGATATGTAATTAAT	780
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Db	781	CGCTGATAAGGCGGAGGTTTGTATATCTTAAATCTCTCTTTGGCCAGAGACTTTG	840
Qy	841	TGTGTGATCTTAAAGTAGACGGAACCTAAGTCAATCTATCTGTTTAAAGACAAAGGTTG	900
Db	841	TGTGTGATCTTAAAGTAGACGGAACCTAAGTCAATCTATCTGTTTAAAGACAAAGGTTG	900
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RESULT 3	
LOCUS	AY964095
DEFINITION	Arabidopsis thaliana isolate N1337 flowering locus C protein mRNA, complete cds.
ACCESSION	AY964095
VERSION	AY964095.1 GI:62632902
KEYWORDS	Arabidopsis thaliana (thale cress)
SOURCE	Arabidopsis thaliana
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 806) Lempe, J., Balasubramanian, S., Sureshkumar, S., Singh, A., Schmid, M. and Weigel, D.
TITLE	Diversity of Flowering Responses in Wild Arabidopsis thaliana
JOURNAL	Strains
PUBMED	PLoS Genet. 1 (1), E6 (2005)
REFERENCE	16103920
AUTHORS	2 (bases 1 to 806) Lempe, J., Balasubramanian, S., Sureshkumar, S., Singh, A., Schmid, M. and Weigel, D.
TITLE	Direct Submission
JOURNAL	Submitted (16-MAR-2005) Department of Molecular Biology, Max Planck Institute for Developmental Biology, Spemannstrasse 37-39, 72076 Tuebingen, Germany
FEATURES	Location/Qualifiers
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		Query Match 84.0%; Score 792; DB 4; Length 806;	
		Best Local Similarity 99.8%; Pred. No. 9.3e-236;	
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Qy	189	GTCTCATCGAGAAAGCTCGTCAGCTTCTGTGTCCTGTGAGCGCATCCGTCGCTTCTCG	248
Db	121	GTCTCATCGAGAAAGCTCGTCAGCTTCTGTGTCCTGTGAGCGCATCCGTCGCTTCTCG	180
Qy	249	TCGTCTCGCTCCGGCAAGCTCTACAGCTTCTCTCGGCGATAAAGCTGTCAGATCC	308
Db	181	TCGTCTCGCTCCGGCAAGCTCTACAGCTTCTCTCGGCGATAAAGCTGTCAGATCC	240
Qy	309	TTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCAGTCAAAAG	368
Db	241	TTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCAGTCAAAAG	300
Qy	369	CTCTGAACATATGTTTACACATATGAGTCTTGAATCTTGTGATGAGCAAGCTTGTGGAT	428
Db	301	CTCTGAACATATGTTTACACATATGAGTCTTGAATCTTGTGATGAGCAAGCTTGTGGAT	360
Qy	429	CAAAATGTCAAAAATGTGAGTATCGATCTCTTGTTCAACTGGAGGAAACACCTTGAGACTG	488
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Qy	489	CCCTCTCGGTGACTAGAGCCAAAGAACCGAATCATGTTGAAAGCTTGTGAGAAATCTTA	548
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Qy	729	ATCCAAACATATATATTAATTAAGAAAGAAAAAATAAGATATGTAATTAATTCGGCTG	786
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Db	721	ATAAGGCGGAGCGTTGTATATCTTAATCTCTCTTGTGCGCCAGAGACTTTGTGTGTG	780
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Db	781	ATACTTAAGTAGCGGAACCTAAGTCA	806	
RESULT 4				
AY964094				
LOCUS	AY964094	806 bp	mRNA	linear
DEFINITION	Arabidopsis thaliana isolate N1273 flowering locus C protein mRNA, complete cds.			
ACCESSION	AY964094	1	GI:62632900	
VERSION	AY964094.1			
KEYWORDS	Arabidopsis thaliana (thale cress)			
SOURCE	Arabidopsis thaliana			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
AUTHORS	1 (bases 1 to 806)			
TITLE	Lempe, J., Balasubramanian, S., Sureshkumar, S., Singh, A., Schmid, M. and Weigel, D.			
JOURNAL	Diversity of Flowering Responses in Wild Arabidopsis thaliana			
PUBMED	Strains			
REFERENCE	PLOS Genet. 1 (1), E6 (2005)			
AUTHORS	16103920			
TITLE	2 (bases 1 to 806)			
JOURNAL	Lempe, J., Balasubramanian, S., Sureshkumar, S., Singh, A., Schmid, M. and Weigel, D.			
FEATURES	Submitted (16-MAR-2005) Department of Molecular Biology, Max Planck Institute for Developmental Biology, Spemannstrasse 37-39, 72076 Tuebingen, Germany			
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Query Match	83.5%; Score 787.2; DB 4; Length 806;			
Best Local Similarity	99.4%; Pred. No. 3e-234;			
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QY	258	CCTCCGGCAAGCTCTACAGCTTCTCCTCCGGGAGTAACCTGGTCAAGATCCTTGTGATCGAT	317	
Db	181	CCTCCGGCAAGCTCTACAGCTTCTCCTCCGGGAGTAACCTGGTCAAGATCCTTGTGATCGAT	240	
QY	318	ATGGGAAACAGCATGCTGATGATCTTAAAGCCCTGGATCATCATGTCAAAGCTCTGAATC	377	
Db	241	ATGGGAAACAGCATGCTGATGATCTTAAAGCCCTGGATCATCATGTCAAAGCTCTGAATC	300	
QY	378	ATGGTTTCACTATGAGTACTTGAACCTTGTGATAGCAAGCTTGTGGATCAAAATGTCA	437	
Db	301	ATGGTTTCACTATGAGTACTTGAACCTTGTGATAGCAAGCTTGTGGATCAAAATGTCA	360	
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QY	498	TGACTAGAGCCCAAGAGACCGAACTCATCTTGAAGCTTGTGAGAAATCTTAAAGAAAAGG	557	
Db	421	TGACTAGAGCCCAAGAGACCGAACTCATCTTGAAGCTTGTGAGAAATCTTAAAGAAAAGG	480	
QY	558	AGAAAATGCTGAAAAGAGAAACCAAGTTTGGCTAGCCAGATGGAGAAATTAATCATCATG	617	
Db	481	AGAAAATGCTGAAAAGAGAAACCAAGTTTGGCTAGCCAGATGGAGAAATTAATCATCATG	540	
QY	618	TGGGAGCAGAACTGAGATGGAGATGTCACTGCTGGCAAAATCTCCGCAATCTTCCCGG	677	
Db	541	TGGGAGCAGAACTGAGATGGAGATGTCACTGCTGGCAAAATCTCCGCAATCTTCCCGG	600	
QY	678	TGACTCTCCACTACTTAATTAGCCACCTTAATCGCGGTTGAAATCAAAATCCAAAAC	737	
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QY	738	ATATATAATTATGAAGA--AAAAAAAATAAGATATGTAATTATTCGCTGATAAGGGCG	795	
Db	661	ATATATAATTATGAAGAAGAAAAAATAAGATATGTAATTATTCGCTGATAAGGGCG	720	
QY	796	ACGGTTTGATATCTTAATACCTCTCTTTGGCCAGAGACTTTGTTGTGTGATACCTTAAG	855	
Db	721	ACGGTTTGATATCTTAATACCTCTCTTTGGCCAGAGACTTTGTTGTGTGATACCTTAAG	780	
QY	856	TAGACGGAACTAAGTCAATACCTCT 881		
Db	781	TAGACGGAACTAAGTCAATACCTCT 806		
RESULT 5				
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LOCUS	BD268759	797 bp	DNA	linear
DEFINITION	Alteration of flowering time in plants.			
ACCESSION	BD268759			
VERSION	BD268759.1		GI:33078527	
KEYWORDS	JP 2002537768-A/1.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
AUTHORS	1 (bases 1 to 797)			
TITLE	Amasino, R.M., Schomburg, F.M., Michaels, S.D., Sung, S.B. and			
JOURNAL	Scortecci, K.			
COMMENT	Alteration of flowering time in plants			
	Patent: JP 2002537768-A 1 12-NOV-2002;			
	WISCONSIN ALUMNI RESEARCH FOUNDATION			
	OS Arabidopsis thaliana (thale cress)			
	PN JP 2002537768-A/1			
	PD 12-NOV-2002			
	PF 25-FEB-2000 JP 2000601179			
	PR 60/121572, 09-MAR-1999 US 60/123455 PI			
	RICHARD MARK AMASINO, FRITZ MICHAEL SCHOMBURG, SCOTT DANIEL PI			
	MICHAELS,			
	PI SI BUM SUNG, KATIA SCORTECCI			
	PC A01H5/00, C12N15/09, C12N15/00			
	CC Alteration of flowering time in plants			
	FH Key Location/Qualifiers			
	FT CDS (1)..(588).			
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	/db_xref="taxon:3702"			
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Query Match		83.2%;	Score 784.4;	DB 2;	Length 797;
Best Local Similarity		99.9%;	Pred. No. 2.2e-233;		
Matches 785;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	110	ATGGGAAGAAAAAACTAGAAATCAAGCGAATTGAGAACAAAGTAGCGCAAGTCACC	169		
Db	1	ATGGGAAGAAAAAACTAGAAATCAAGCGAATTGAGAACAAAGTAGCGCAAGTCACC	60		
Qy	170	TTCTCCAAACGTGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGAC	229		
Db	61	TTCTCCAAACGTGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGAC	120		
Qy	230	GCATCCGTCGCTCTTCTCGTCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC	289		
Db	121	GCATCCGTCGCTCTTCTCGTCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC	180		
Qy	290	GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCC	349		
Db	181	GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCC	240		
Qy	350	TTGGATCATCAGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTGTG	409		
Db	241	TTGGATCATCAGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTGTG	300		
Qy	410	GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACCTG	469		
Db	301	GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACCTG	360		
Qy	470	GAGGAACACCTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAACCGAACTCATGTTG	529		
Db	361	GAGGAACACCTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAACCGAACTCATGTTG	420		
Qy	530	AAGCTTGTGAGATCTTAAAGAAAGAGGAAATGCTGAAAGAGAGAACAGAGTTTGTG	589		
Db	421	AAGCTTGTGAGATCTTAAAGAAAGAGGAAATGCTGAAAGAGAGAACAGAGTTTGTG	480		
Qy	590	GCTAGCCAGATGGAGAAATCAATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCT	649		
Db	481	GCTAGCCAGATGGAGAAATCAATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCT	540		
Qy	650	GCTGGACAAATCTCCGCAATCTTCCGCTGACTCTCCCACTACTTAATAGCCACCTTAA	709		
Db	541	GCTGGACAAATCTCCGCAATCTTCCGCTGACTCTCCCACTACTTAATAGCCACCTTAA	600		
Qy	710	ATCGGCGTTGAAATCAAAATCCAAACATATATAATTAATGAAGAAAAAAATAAGAT	769		
Db	601	ATCGGCGTTGAAATCAAAATCCAAACATATATAATTAATGAAGAAAAAAATAAGAT	660		
Qy	770	ATGTAATTTATTCGCTGATAGGGGAGCGTTGTATATCTTAATACCTCTCTTTGGCC	829		
Db	661	ATGTAATTTATTCGCTGATAGGGGAGCGTTGTATATCTTAATACCTCTCTTTGGCC	720		
Qy	830	AAGAGACTTTGTGTGATCTTAAAGTAGCGGAACCTAAGTCAATATCTATCTGTTTAAAG	889		
Db	721	AAGAGACTTTGTGTGATCTTAAAGTAGCGGAACCTAAGTCAATATCTATCTGTTTAAAG	780		
Qy	890	ACAAAA 895			
Db	781	ACAAAA 786			

RESULT 6
AR476092
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AR476092
Sequence 1 from patent US 6693228.
AR476092
AR476092.1 GI:42716039
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 797)
Anasino,R.M., Schomburg,P.M., Michaels,S.D., Sung,S.-B. and

Scortecci,K.		Alteration of flowering time in plants	
Patent: US 6693228-A 1 17-FEB-2004;		Wisconsin Alumni Research Foundation; Madison, WI	
Location/Qualifiers		1..797	
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ORIGIN		/mol_type="genomic DNA"	
Query Match		83.2%;	Score 784.4;
Best Local Similarity		99.9%;	Pred. No. 2.2e-233;
Matches 785;		Conservative 0;	Mismatches 1;
		Indels 0;	Gaps 0;
Qy	110	ATGGGAAGAAAAAACTAGAAATCAAGCGAATTGAGAACAAAGTAGCGCAAGTCACC	169
Db	1	ATGGGAAGAAAAAACTAGAAATCAAGCGAATTGAGAACAAAGTAGCGCAAGTCACC	60
Qy	170	TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTTCTCTGTGAC	229
Db	61	TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTTCTCTGTGAC	120
Qy	230	GCATCCGTCGCTCTTCTCGTCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCCGGC	289
Db	121	GCATCCGTCGCTCTTCTCGTCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCCGGC	180
Qy	290	GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCC	349
Db	181	GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCC	240
Qy	350	TTGGATCATCATGTCAGAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAATTGTG	409
Db	241	TTGGATCATCATGTCAGAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAATTGTG	300
Qy	410	GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACCTG	469
Db	301	GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACCTG	360
Qy	470	GAGGAACACCTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAACCGAACTCATGTTG	529
Db	361	GAGGAACACCTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAACCGAACTCATGTTG	420
Qy	530	AAGCTTGTGAGATCTTAAAGAAAGAGGAAATGCTGAAAGAGAGAACAGAGTTTGTG	589
Db	421	AAGCTTGTGAGATCTTAAAGAAAGAGGAAATGCTGAAAGAGAGAACAGAGTTTGTG	480
Qy	590	GCTAGCCAGATGGAGAAATCAATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCT	649
Db	481	GCTAGCCAGATGGAGAAATCAATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCT	540
Qy	650	GCTGGACAAATCTCCGCAATCTTCCGCTGACTCTCCCACTACTTAATAGCCACCTTAA	709
Db	541	GCTGGACAAATCTCCGCAATCTTCCGCTGACTCTCCCACTACTTAATAGCCACCTTAA	600
Qy	710	ATCGGCGTTGAAATCAAAATCCAAACATATATAATTAATGAAGAAAAAAATAAGAT	769
Db	601	ATCGGCGTTGAAATCAAAATCCAAACATATATAATTAATGAAGAAAAAAATAAGAT	660
Qy	770	ATGTAATTTATTCGCTGATAGGGGAGCGTTGTATATCTTAATACCTCTCTTTGGCC	829
Db	661	ATGTAATTTATTCGCTGATAGGGGAGCGTTGTATATCTTAATACCTCTCTTTGGCC	720
Qy	830	AAGAGACTTTGTGTGATCTTAAAGTAGCGGAACCTAAGTCAATATCTATCTGTTTAAAG	889
Db	721	AAGAGACTTTGTGTGATCTTAAAGTAGCGGAACCTAAGTCAATATCTATCTGTTTAAAG	780
Qy	890	ACAAAA 895	
Db	781	ACAAAA 786	
RESULT 7		AF537203	

LOCUS	AF537203	801 bp	mRNA	linear	PLN 02-SEP-2002
DEFINITION	Arabidopsis thaliana flowering locus C protein mRNA, complete cds.				
ACCESSION	AF537203				
VERSION	AF537203.1	GI:22653433			
KEYWORDS					
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	1. (bases 1 to 801)				
AUTHORS	Michaelis, S.D. and Amasino, R.M.				
TITLE	FLOWERING LOCUS C encodes a novel MADS domain protein that acts as a repressor of flowering				
JOURNAL	Plant Cell 11 (5), 949-956 (1999)				
PUBMED	10330478				
REFERENCE	2. (bases 1 to 801)				
AUTHORS	Michaelis, S.D. and Amasino, R.M.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-AUG-2002) Biochemistry, University of Wisconsin-Madison, 433 Babcock Drive, Madison, WI 53706, USA				
FEATURES	Location/Qualifiers				
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Query Match	83.2%; Score 784.4; DB 4; Length 801;				
Best Local Similarity	99.9%; Pred. No. 2.2e-233;				
Matches	785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	110	ATGGGAAGAAAAAATAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAAAGTCACC	169		
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QY	170	TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGAC	229		
DB	61	TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGAC	120		
QY	230	GCATCGCTCGCTTCTGTCGTCTCGGCTCCGGCAAGCTCTACAGCTTCTCTCTCGGC	289		
DB	121	GCATCGCTCGCTTCTGTCGTCTCGGCTCCGGCAAGCTCTACAGCTTCTCTCTCGGC	180		
QY	290	GATAACCTGTCAGATCCTTCATCGATATGGAACAGCATGCTGATCTTAAAGCC	349		
DB	181	GATAACCTGTCAGATCCTTCATCGATATGGAACAGCATGCTGATCTTAAAGCC	240		
QY	350	TTGGATCATCAGTCAAAAGCTCTGAACATATGTTTCACTATGAGCTACTTGAACCTTGTG	409		
DB	241	TTGGATCATCAGTCAAAAGCTCTGAACATATGTTTCACTATGAGCTACTTGAACCTTGTG	300		
QY	410	GATAGCAAGCTTGTGGATCAAAATGTCAAAAATGTGAGTATCGATGCTTGTTCAACTG	469		
DB	301	GATAGCAAGCTTGTGGATCAAAATGTCAAAAATGTGAGTATCGATGCTTGTTCAACTG	360		
QY	470	GAGGAACACTTGTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGACCGAAGCTCATGTTG	529		
DB	361	GAGGAACACTTGTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGACCGAAGCTCATGTTG	420		
QY	530	AAGCTTTGTTGAGAAATCTTAAAGAAAGGAGAAAAATGCTGAAAGAGAACCAAGCTTTTG	589		
Db	421	AAAGCTTTGTTGAGAAATCTTAAAGAAAGGAGAAAAATGCTGAAAGAGAACCAAGCTTTTG	480		
QY	590	GCTAGCCAGATGGAGAAATATCATCATGTGGAGAGCAAGCTGAGATGGAGATGTACCT	649		
DB	481	GCTAGCCAGATGGAGAAATATCATCATGTGGAGAGCAAGCTGAGATGGAGATGTACCT	540		
QY	650	GCTGGACAAATCTCCGACAAATCTTCCGGTGACTCTCCCACTACTTAAATAGCCACCTTAA	709		
DB	541	GCTGGACAAATCTCCGACAAATCTTCCGGTGACTCTCCCACTACTTAAATAGCCACCTTAA	600		
QY	710	ATCGCGGTTGAAATCAAATCCAAACATATATTAATTAAGAAAAAATAAAGAT	769		
DB	601	ATCGCGGTTGAAATCAAATCCAAACATATATTAATTAAGAAAAAATAAAGAT	660		
QY	770	ATGTAATTAATTCGGCTGATAGAGCGGAGGTTGTATATCTTAATCTCTCTTTGGCC	829		
DB	661	ATGTAATTAATTCGGCTGATAGAGCGGAGGTTGTATATCTTAATCTCTCTTTGGCC	720		
QY	830	AAGAGACTTTGTGTGTGACTTAAGTAGACGAAGCTAAAGTCAATCTATCTGTTTTAAG	889		
DB	721	AAGAGACTTTGTGTGTGACTTAAGTAGACGAAGCTAAAGTCAATCTATCTGTTTTAAG	780		
QY	890	ACAAAA 895			
DB	781	ACAAAA 786			
RESULT 8					
AY850001	774 bp mRNA linear PLN 03-AUG-2005				
LOCUS	Arabidopsis thaliana ecotype Van-0 flowering locus C protein (FLC)				
DEFINITION	mRNA, complete sequence, alternatively spliced.				
ACCESSION	AY850001				
VERSION	AY850001.1 GI:61661329				
KEYWORDS	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	1. (bases 1 to 774)				
AUTHORS	Werner, J.D., Borevitz, J.O., Uhlenhaut, N.H., Ecker, J.R., Chory, J. and Weigel, D.				
TITLE	FRIGIDA-Independent Variation in Flowering Time of Natural Arabidopsis thaliana Accessions				
JOURNAL	Genetics 170 (3), 1197-1207 (2005)				
PUBMED	15911588				
REFERENCE	2. (bases 1 to 774)				
AUTHORS	Werner, J.D., Borevitz, J.O., Uhlenhaut, N.H., Ecker, J.R., Chory, J. and Weigel, D.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-DEC-2004) Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Rd., La Jolla, CA 92037, USA				
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	/ecotype="Van-0"				
gene	1..774				
	/gene="FLC"				
	/note="flowering locus C protein; loss-of-function allele; contains premature stop codon in exon 6"				
ORIGIN					
Query Match	81.7%; Score 770.8; DB 4; Length 774;				
Best Local Similarity	99.7%; Pred. No. 3.9e-229;				
Matches	772; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				

QY 599 -----ATGAGAAATATCATCTGTGGG 622
 Db 601 AGTGNATAGTATTTGACCTATGATTATCGTACATGAGGAAATATCATCTGTGGG 660
 QY 623 GCAGAGCTGAGATGGAGATGTCACTGCTGGACAAATCTCCGACAACTTCCGGTGA 682
 Db 661 GCAGAGCTGAGATGGAGATGTCACTGCTGGACAAATCTCCGACAACTTCCGGTGA 720
 QY 683 CTCCCACTACTTAATTAGCCACCTTAATCTGGCGGTTGAAATCAAATCCAAAACATATA 742
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 QY 743 TAATTATGAAGA--AAAAAATAAGATATGTAATTATTCCGTGATGAAGGCGAGCGT 800
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 QY 801 TT 802
 Db 841 TT 842

RESULT 10
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 LOCUS
 DEFINITION Arabidopsis thaliana ecotype Van-0 flowering locus C protein (FLC)
 mRNA, complete cds, alternatively spliced.
 ACCESSION AY850002
 VERSION
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 732)
 AUTHORS Werner, J.D., Borevitz, J.O., Uhlenhaut, N.H., Ecker, J.R., Chory, J.
 and Weigel, D.
 TITLE FRIGIDA-Independent Variation in Flowering Time of Natural
 Arabidopsis thaliana Accessions
 JOURNAL Genetics 170 (3), 1197-1207 (2005)
 PUBMED 15911588
 REFERENCE 2 (bases 1 to 732)
 AUTHORS Werner, J.D., Borevitz, J.O., Uhlenhaut, N.H., Ecker, J.R., Chory, J.
 and Weigel, D.
 TITLE Direct Submission
 JOURNAL Submitted (08-DEC-2004) Plant Biology Laboratory, The Salk
 Institute for Biological Studies, 10010 N. Torrey Pines Rd., La
 Jolla, CA 92037, USA
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 82..630
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 /notes="alternatively spliced; transcript lacks exon 6"
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 /protein_id="AAK51271.1"
 /db_xref="GI:61661331"
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gene
 CDS

Query Match 72.1%; Score 680; DB 4; Length 732;

ORIGIN

Best Local Similarity 94.6%; Pred. No. 9.5e-201;
 Matches 732; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

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 QY 89 AAGCCCTCTCGGAGAGAGCCATGGGAAGAAAAAATAGAAATCAAGCCAAATTGAGAAC 148
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 QY 149 AAAAGTAGCCGACCACTTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGT 208
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 QY 209 CAGCTTTCTGTTCTCTGTGACGATCCGTCGCTCTTCTGTCGTCCTCCGCTCCGGCAAG 268
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 QY 389 TATGAGCTACTTGAACCTTGTGGATAGCAAGCTTGTGGATCAAAATGTCAAAATGTGAGT 448
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 QY 449 ATCGATGCTCTGTTCACACTGGGAGAACACTTGAGACTGCCCTCTCCGTCGACTAGAGCC 508
 Db 421 ATCGATGCTCTGTTCACACTGGGAGAACACTTGAGACTGCCCTCTCCGTCGACTAGAGCC 480
 QY 509 AAGAAGACCGAACTCATGTTTGAAGCTTGTGAGAATCTTAAAGAAAGGAGAAATGCTG 568
 Db 481 AAGAAGACCGAACTCATGTTTGAAGCTTGTGAGAATCTTAAAGAAAGGAGAAATGCTG 526
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 Db 527 -----AGATGGAGAAATATCATATGTGGGAGCAGAA 558
 QY 629 GCTGAGATGGAGATGTCACCTGCTGGACAAATCTCCGACAACTCTCCGTCGACTCTCCCA 688
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 Db 679 TGAAGAAAAAATAAGATATGTAATTATTCGCTGATGAAGGCGAGCGTTT 732

RESULT 11
 DQ167446
 LOCUS
 DEFINITION Arabidopsis arenosa MADS-box flowering locus C (FLC1) mRNA,
 complete cds.
 ACCESSION DQ167446
 VERSION
 KEYWORDS
 SOURCE Arabidopsis arenosa
 ORGANISM Arabidopsis arenosa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 651)
 AUTHORS Wang, J., Tian, L., Lee, H.-S. and Chen, Z.J.
 TITLE Sequence evolution, epigenetic regulation, and trans-acting effects
 mediate FLC expression and flowering-time variation in Arabidopsis

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

allopolyploids
Unpublished
2 (bases 1 to 651)
Wang,J., Tian,L., Lee,H.-S. and Chen,Z.J.
Direct Submission
Submitted (15-AUG-2005) Soil & Crop Sciences, Texas A&M University,
610 Heep Center, College Station, TX 77843, USA
Location/Qualifiers
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/mol_type="mRNA"
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ORIGIN

Query Match 63.0%; Score 593.8; DB 4; Length 651;
Best Local Similarity 95.5%; Pred. No. 8.3e-174;
Matches 622; Conservative 0; Mismatches 27; Indels 2; Gaps 1;

Qy 76 AAATAGGGCAAAAGCCCTTCGGAG--AGAAGCCATGGGAAGAAAAAAGTGAATC 133
Db 1 AAATAGGGCAAAAGCCCTTCGGAGACAGAGCCATGGGAGTAAAGAACTAGAATC 60
Qy 134 AAGCGAATTGAGAACAAAGTAGCGGACAGTCACTTCTCCAAACGTCGCAACGCTC 193
Db 61 AAGCGAATTGAGAACAAAGTAGCGGACAGTCACTTCTCCAAACGTCGCAACGCTC 120
Qy 194 ATCGAGAAAGCTGTCAGCTTCTGTTCTGTGACGATCGTGGCTTCTTCTGTCGTC 253
Db 121 ATCGAGAAAGCTGTCAGCTTCTGTTCTGTGACGATCGTGGCTTCTTCTGTCGTC 180
Qy 254 TCCGCTCCGGCAGCTCTACAGCTTCTTCCGGCAGATACCTGGTCAAGATCCTTGAT 313
Db 181 TCCGCTCCGGCAGCTCTACAGCTTCTTCCGGCAGATACCTGGTCAAGATCCTTGAT 240
Qy 314 CGATATGGGAAACAGCATGCTGATGATCTTAAAGCCCTTGGATCATCATGCAAGCTCTG 373
Db 241 CGATATGGGAAACAGCATGCTGATGATCTTAAAGCCCTTGGATCATCATGCAAGCTCTG 300
Qy 374 AACTATGGTTTCACTATGAGCTACTTGAACCTTGTGGATAGCAAGCTTGTGGATCAAT 433
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Qy 434 GTCAAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 493
Db 361 GTCAAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 494 TCCGTGACTAGCCAGAGAGACCGAATCATGTTGTAAGCTTGTGAGATCTTTAAAGAA 553
Db 421 TCCGTGACTAGCCAGAGAGACCGAATCATGTTGTAAGCTTGTGAGATCTTTAAAGAA 480
Qy 554 AAGGAGAAAAATGCTGAAAGAGAGAACAGGCTTGTGGCTAGCCAGATGGAGAAATATCAT 613
Db 481 AAGGAGAAAAATGCTGAAAGAGAGAACAGGCTTGTGGCTAGCCAGATGGAGAAATATCAT 540
Qy 614 CATGTGGGAG 673
Db 541 CATGTGGGAG 600
Qy 674 CCGGTGACTCTCCCACTACTTAATTAGCCACCTTAATTCGGCGGTGAAT 724

Db 601 CCGGTGACTCTCCGCTCTTAATTAGCCACCTTAATTCGGCGGTGAAT 651

RESULT 12
AY964092
LOCUS
DEFINITION
Arabidopsis thaliana isolate N1203 flowering locus C protein mRNA,
complete cds.
ACCESSION
AY964092
VERSION
AY964092.1
KEYWORDS
GI:62632896
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
REFERENCE
1 (bases 1 to 591)
Lempe,J., Balasubramanian,S., Sureshkumar,S., Singh,A., Schmid,M.
and Weigel,D.
Diversity of Flowering Responses in Wild Arabidopsis thaliana
Strains
PLoS Genet. 1 (1), E6 (2005)
16103920
2 (bases 1 to 591)
Lempe,J., Balasubramanian,S., Sureshkumar,S., Singh,A., Schmid,M.
and Weigel,D.
Direct Submission
Submitted (16-MAR-2005) Department of Molecular Biology, Max Planck
Institute for Developmental Biology, Spemannstrasse 37-39, 72076
Tuebingen, Germany
Qualifiers
1..591
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/isolate="N1203"
/db_xref="taxon:3702"
/ecotype="Gr-3"
1..591
/codon_start=1
/product="flowering locus C protein"
/protein_id="AAK89409.1"
/db_xref="GI:62632897"
/translation="MGRKLEIKRIENKSRQVTFKRRNGLIEKARQLSVLCDA
SV
LLVVSAGKLYSFSGDNLVKIDRYGKHADDLKALDIOSKALNYSHLELLELVS
KLVSNNKYNVSDTLVLEHGLTALSVTAKTELMLKLVENLKEKELKAEQV
ASQMKNNHHVGAEMEMSPAGQISDNLPTVLP
ORIGIN

Query Match 62.7%; Score 591; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.2e-173;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 ATCGGAGAAAAAAGCTAGAAATCAAGCAATTCAGAACAAAGTAGCCGCAAGTCAAC 169
Db 1 ATCGGAGAAAAAAGCTAGAAATCAAGCAATTCAGAACAAAGTAGCCGCAAGTCAAC 60
Qy 170 TTCTCCAAAGCTGCCAACGCTCTCATCGAGAAAGCTCGTCAGCTTCTCTGTGAC 229
Db 61 TTCTCCAAAGCTGCCAACGCTCTCATCGAGAAAGCTCGTCAGCTTCTCTGTGAC 120
Qy 230 GCATCGCTGCTCTTCTGCTGCTCGCTCGCTCGGCAAGCTCTACAGCTTCTCTCGGC 289
Db 121 GCATCGCTGCTCTTCTGCTGCTCGCTCGCTCGGCAAGCTCTACAGCTTCTCTCGGC 180
Qy 290 GATAACCTGTCAGATCCCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 349
Db 181 GATAACCTGTCAGATCCCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 240
Qy 350 TTGGATCATCAGTCAAAAGCTCTGAATATGTTTCACTATGAGCTTCTGAACTTGTG 409
Db 241 TTGGATCATCAGTCAAAAGCTCTGAATATGTTTCACTATGAGCTTCTGAACTTGTG 300
Qy 410 GATAGCAAGCTTGTGGATCAAAATGTGAGTATGATGATGATGATGATGATGATGATGAT 469

Search completed: May 22, 2006, 07:02:51
Job time : 5456 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 05:20:17 ; Search time 645 Seconds
(without alignments)
10193.535 Million cell updates/sec

Title: US-09-857-346A-2
Perfect score: 943
Sequence: 1 cgagaaaggagaaaaaa.....tgagaaaaaa 943

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 8:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*
- 15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943	100.0	943	3	AAA29031 A. thalia
2	943	100.0	943	4	AAF80398 Nucleotid
3	943	100.0	943	10	ADD30735 Plant yie
4	943	100.0	943	12	ADI43666 Plant tra
5	943	100.0	943	12	ADO03460 Thalecres
6	784.4	83.2	797	3	AAA28120 Arabidops
7	746	79.1	758	3	AAC39385 Arabidops
8	591	62.7	591	14	AEBA7394 Arabidops
9	538.4	57.1	868	3	AAA29035 B. napus
10	528	56.0	845	3	AAA29039 B. napus
11	527	55.9	891	3	AAA29041 B. napus
12	494.8	52.5	969	3	AAA29034 B. napus
13	491.8	52.2	851	13	ADW76669 Chinese c
14	490.8	52.0	825	3	AAA29040 B. napus
15	484	51.3	990	3	AAA29037 B. napus
16	477.4	50.6	908	3	AAA29032 B. napus
17	471.4	50.0	780	3	AAA29038 B. napus
18	468.4	49.7	847	3	AAA29033 B. napus

19	464.2	49.2	792	3	AAA29036 B. napus
20	448.6	47.6	867	3	AAA28124 Brassica
21	439	46.6	863	3	AAA28123 Brassica
22	373.6	39.6	884	3	AAC38871 Arabidops
23	373.6	39.6	884	15	AEF28378 Lead_Cere
24	372.6	39.5	883	4	AAF80385 Nucleotid
25	372.6	39.5	883	10	ADD31054 Plant yie
26	372.6	39.5	883	12	ADI41552 Plant tra
27	372.6	39.5	883	12	ADO01656 Thalecres
28	372.6	39.5	883	12	ADO03320 Thalecres
29	363.8	38.6	1059	4	AAF80389 Nucleotid
30	363.8	38.6	1059	10	ADD31022 Plant yie
31	363.8	38.6	1059	12	ADI41886 Plant tra
32	363.8	38.6	1059	12	ADO03468 Thalecres
33	363.8	38.6	1059	12	ADO02530 Thalecres
34	362.6	38.5	1036	4	AAF80388 Nucleotid
35	362.6	38.5	1036	10	ADD31076 Plant yie
36	362.6	38.5	1036	12	ADI41702 Plant tra
37	362.6	38.5	1036	12	ADO02154 Thalecres
38	362.6	38.5	1036	12	ADO03398 Thalecres
39	360.6	38.2	604	10	ADK53672 Plant DNA
40	347	36.8	877	13	ADK45436 Plant ful
41	342	36.3	591	8	ABZ42141 Arabidops
42	339.6	36.0	610	12	ADO03536 Thalecres
43	336.6	35.7	537	10	ADK55986 Plant DNA
44	334	35.4	5968	14	ABE47395 Arabidops
45	324.4	34.4	687	12	ADG47881 Arabidops

ALIGNMENTS

RESULT 1

AAA29031 standard; DNA; 943 BP.

XX AAA29031;
AC AAA29031;

DT 12-SEP-2000 (first entry)

DE A. thaliana flowering locus F (FLF) cDNA.

XX Flowering locus F; transcription factor; DNA binding domain; MADS box;
KW FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.

OS Arabidopsis thaliana.

XX Key Location/Qualifiers
FH CDS 110..700

FT /*tag= a

FT /product= "MADS_box_protein"

FT /note= "encodes a transcription factor comprising a

FT distinctive DNA binding domain"

XX WO200032780-A1.

XX 08-JUN-2000.

XX 02-DEC-1999; 99WO-AU001079.

XX 03-DEC-1998; 98AU-00007469.

XX 22-JAN-1999; 99US-0116928P.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX (PERE/) PEREZ P.

XX Perez P, Burn JE, Peacock WJ, Dennis ES, Sheldon CC;

XX Helliwell CA, Rouse DT;

XX WPI; 2000-451762/39.

XX P-PSDB; AAY96407.

XX New nucleic acid comprising a MADS box that encodes a transcription

factor for altering the flowering time or modifying the vegetative or floral phenotype of a plant such as wheat.

Claim 6; Page 83; 106pp; English.

The present cDNA, isolated from *Arabidopsis thaliana*, encodes a transcription factor protein comprising a distinct conserved DNA binding domain (a MADS box). The DNA was identified from a late-flowering mutant (C24), which arose during transformation of the early-flowering ecotype C24 with a modified binary vector pBIN-delta-Ac. This vector contains the neomycin phosphotransferase II (NPTII) gene under the control of the nopaline synthase (NOS) promoter, together with a deleted maize Ac transposable element inserted within the untranslated leader of the beta-glucuronidase gene, in the reverse orientation to the direction of transcription. It was found that two T-DNA segments in the very late flowering phenotype and that two expressed genes (A and B) were closely linked to these T-DNAs. Gene B was re-designated as FLF. The FLF gene is linked to the top of chromosome 5, 4 cm from RFLP marker 447. The protein is capable of altering the flowering time of a plant. Over-expression of the FLF gene can be used to delay flowering in a plant. Alternatively, reduction of FLF gene expression, e.g. by antisense constructs, can be used to induce early flowering. Methods of modifying vegetative and/or floral phenotypes of a plant comprising increasing the level of expression of a FLF gene to modify the production or activity of a gibberellin in the plant are also claimed. The response of a plant to vernalization can also be altered. Any dicotyledonous or monocotyledonous plant species including horticultural plants, particularly those in the cut-flower industry, vegetable, cereal and other crop plants are capable of being controlled.

Sequence 943 BP; 319 A; 193 C; 203 G; 228 T; 0 U; 0 Other;

Query Match 100.0%; Score 943; DB 3; Length 943;
Best Local Similarity 100.0%; Pred No. 1.2e-240; Indels 0; Gaps 0;
Matches 943; Conservative 0; Mismatches 0;

QY 1 CGAGAAAGGAAAAAATAAGAGAGAAACGCTTAGTATCTCCGGCGACTTGAAC 60
DB 1 CGAGAAAGGAAAAAATAAGAGAGAAACGCTTAGTATCTCCGGCGACTTGAAC 60
QY 61 CCAACCTGAGGATCAAAATTAGGGCAAAAGCCCTCTCGGAGAGAGCCATGGGAAGAA 120
DB 61 CCAACCTGAGGATCAAAATTAGGGCAAAAGCCCTCTCGGAGAGAGCCATGGGAAGAA 120
QY 121 AAACTAGAAATCAAGCGAATTCAGAACAAAGTAGCCGACAGTCACTTCTCCAAACG 180
DB 121 AAACTAGAAATCAAGCGAATTCAGAACAAAGTAGCCGACAGTCACTTCTCCAAACG 180
QY 181 TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTGACGCAATCCGTCGC 240
DB 181 TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTGACGCAATCCGTCGC 240
QY 241 TCTTCTGTCGCTCCGGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGAATCACTGGT 300
DB 241 TCTTCTGTCGCTCCGGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGAATCACTGGT 300
QY 301 CAAGATCTTGTATGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA 360
DB 301 CAAGATCTTGTATGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA 360
QY 361 GTCAAAAGCTCTGAACATATGGTTTCAACATATGAGCTACTTGAACCTTGTGATAGCAAGCT 420
DB 361 GTCAAAAGCTCTGAACATATGGTTTCAACATATGAGCTACTTGAACCTTGTGATAGCAAGCT 420
QY 421 TGTGGATCAAAATGTCAAAATGTAGATTCGATGCTCTTGTTCATCTGAGGAAACCT 480
DB 421 TGTGGATCAAAATGTCAAAATGTAGATTCGATGCTCTTGTTCATCTGAGGAAACCT 480
QY 481 TGAGACTGCGCTCTCCGCTAGACCAAGAGACGCAACTCATCTGTAAGCTTCTTGA 540
DB 481 TGAGACTGCGCTCTCCGCTAGACCAAGAGACGCAACTCATCTGTAAGCTTCTTGA 540
QY 541 GAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAAACAGGTTTTGGCTAGCCAGAT 600

DB 541 GAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAAACAGGTTTTGGCTAGCCAGAT 600
QY 601 GGAGATAATCATCATGTGGAGCAGAACTGAGATGGAGATGTCACTGCTGGACAAAT 660
DB 601 GGAGATAATCATCATGTGGAGCAGAACTGAGATGGAGATGTCACTGCTGGACAAAT 660
QY 661 CTCGGCAATCTTCCGGTGACTCTCCACTACTTAAATAGCCACCTTAAATCGCGGTTG 720
DB 661 CTCGGCAATCTTCCGGTGACTCTCCACTACTTAAATAGCCACCTTAAATCGCGGTTG 720
QY 721 AAATCAAAATCCAAACATATATAATTAAGAGAAAAAATAAGATATGTAATATT 780
DB 721 AAATCAAAATCCAAACATATATAATTAAGAGAAAAAATAAGATATGTAATATT 780
QY 781 CCGCTGATAGGGCGAGCGTTTGTATATCTTAACTCTCTTTGGCCAGAGACTTTG 840
DB 781 CCGCTGATAGGGCGAGCGTTTGTATATCTTAACTCTCTCTTTGGCCAGAGACTTTG 840
QY 841 TGTGTGATACTTAAAGTAGACGGAACCTAAGTCAATCTATCTGTTTTAAGCAAAAGTTG 900
DB 841 TGTGTGATACTTAAAGTAGACGGAACCTAAGTCAATCTATCTGTTTTAAGCAAAAGTTG 900
QY 901 ATGAACCTTTGTACCTTATTCGTGTGAGAAAAAATAAGAAAAA 943
DB 901 ATGAACCTTTGTACCTTATTCGTGTGAGAAAAAATAAGAAAAA 943
RESULT 2
AAF80398
ID AAF80398 standard; cDNA; 943 BP.
XX
AC AAF80398;
XX 29-JUN-2001 (first entry)
DE Nucleotide sequence of a plant transcription factor G1759.
KW Transcription factor; flowering time; transgenic plant; vernalisation;
KW plant development; plant physiology; flowering; ss.
OS *Arabidopsis thaliana*.
FH Key Location/Qualifiers
FT CDS 110..700
FT /*tag= a
FT /product= "transcription factor"
XX WO200126459-A2.
PN 19-APR-2001.
XX 11-OCT-2000; 2000WO-US028141.
XX 12-OCT-1999; 99US-0159464P.
PR 08-NOV-1999; 99US-0164132P.
PR 17-NOV-1999; 99US-0166228P.
PR 17-APR-2000; 2000US-0197899P.
PR 22-AUG-2000; 2000US-0227439P.
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (RATC/) RATCLIFFE O.
PA (HEAR/) HEARD J.
PA (SAMA/) SAMAHA R.
PA (CREE/) CREELMAN R.
PA (KEDD/) KEDDIE J.
PA (JIAN/) JIANG C.
PA (REUB/) REUBER L.
PA (RIEC/) RIECHMANN J L.
XX Ratcliffe O, Heard J, Samaha R, Creelman R, Keddie J, Jiang C;
PI Reuber L, Riechmann JL;

DR WPI; 2001-266398/27.
DR P-PSDB; AAB67828.
XX
PT New transgenic plant comprises a recombinant polynucleotide encoding a
PT plant transcription factor polypeptide and has a modified flowering time
PT or vernalization requirement.
XX
PS Example 1; Page 67-68; 108pp; English.
XX
CC The present sequence encodes a plant transcription factor protein which
CC modifies the flowering time of a plant. The polynucleotide sequence is
CC used to produce transgenic plants which have a modified flowering time or
CC a modified vernalization requirement. The polynucleotides and
CC polypeptides are useful for modifying plant development, physiology or
CC biochemistry such that the modified plants have a trait advantage over
CC wild type plants. In particular they are useful for accelerating,
CC delaying or preventing flowering. The polynucleotides are also useful as
CC nucleic acid probes and primers. They may be used to identify proteins
CC that can modify the activity of the transcription factor
XX
SQ Sequence 943 BP; 319 A; 193 C; 203 G; 228 T; 0 U; 0 Other;
Query Match 100.0%; Score 943; DB 4; Length 943;
Best Local Similarity 100.0%; Pred. No. 1.2e-240;
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGAAAGGAAAAAATAGAAAGAGAAACGCTTAGTATCTCCGGCGACTTGAAC 60
Db 1 CGAGAAAGGAAAAAATAGAAAGAGAAACGCTTAGTATCTCCGGCGACTTGAAC 60
QY 61 CCAACCTGAGGATCAAAATTAGGACCAAAAGCCCTCTCGAGAGAACCATGGGAAGAA 120
Db 61 CCAACCTGAGGATCAAAATTAGGACCAAAAGCCCTCTCGAGAGAACCATGGGAAGAA 120
QY 121 AAAACTAGAAATCAAGCGAAATGAGACAAAGTAGCCGACAACTTCTCCAAACG 180
Db 121 AAAACTAGAAATCAAGCGAAATGAGACAAAGTAGCCGACAACTTCTCCAAACG 180
QY 181 TCGAACGGTCTCATCGAGAAAGCTCGTCACTTCTCTGTGACGATCGTCGC 240
Db 181 TCGAACGGTCTCATCGAGAAAGCTCGTCACTTCTCTGTGACGATCGTCGC 240
QY 241 TCTTCTGCTGCTCCGGCTCCGCAAGCTCTACAGCTTCTCCTCCGGCGATACCTGGT 300
Db 241 TCTTCTGCTGCTCCGGCTCCGCAAGCTCTACAGCTTCTCCTCCGGCGATACCTGGT 300
QY 301 CAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCTTTGGATCATCA 360
Db 301 CAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCTTTGGATCATCA 360
QY 361 GTCAAAAGCTCTGAATATGTTTCACTATGAGCTACTTGAACCTTGTGGATAGCAAGCT 420
Db 361 GTCAAAAGCTCTGAATATGTTTCACTATGAGCTACTTGAACCTTGTGGATAGCAAGCT 420
QY 421 TGTGGATCAAACTCAAAATGAGTATCGATGCTTCTTCTCACTGGAGGAAACCT 480
Db 421 TGTGGATCAAACTCAAAATGAGTATCGATGCTTCTTCTCACTGGAGGAAACCT 480
QY 481 TGAGACTGCCCTCTCCGTGACTAGAGCAAGACGCACTCATGTTTGAAGCTTTGTGA 540
Db 481 TGAGACTGCCCTCTCCGTGACTAGAGCAAGACGCACTCATGTTTGAAGCTTTGTGA 540
QY 541 GAATCTTAAAGAAAGAGAAAAATGCTGAAAGAGAGAACAGGTTTTGGTACCCAGAT 600
Db 541 GAATCTTAAAGAAAGAGAAAAATGCTGAAAGAGAGAACAGGTTTTGGTACCCAGAT 600
QY 601 GGAGAAATCATCATCTGGAGCAGAGCTGAGATGAGATGTCACCTGCTGACAAAT 660
Db 601 GGAGAAATCATCATCTGGAGCAGAGCTGAGATGAGATGTCACCTGCTGACAAAT 660
QY 661 CTCGCAAACTCTCCGGTGAATCTCCCACTACTTAAATTAGCCACTTTAAATCGCGGTTG 720
Db 661 CTCGCAAACTCTCCGGTGAATCTCCCACTACTTAAATTAGCCACTTTAAATCGCGGTTG 720

QY 721 AAATCAAAATCCAAACATATATATTAATATGAAGAAAAAATAAGATATGTAATATT 780
Db 721 AAATCAAAATCCAAACATATATATTAATATGAAGAAAAAATAAGATATGTAATATT 780
QY 781 CGCTGATAAGCGCGGCTTGTATATCTTAATATCTCTCTCTTGGCCAGAGACTTTG 840
Db 781 CGCTGATAAGCGCGGCTTGTATATCTTAATATCTCTCTCTTGGCCAGAGACTTTG 840
QY 841 TGTGTGATCTTAACTAGTAGACGGAACCTAAGTCAATATCTCTCTTAAAGCAAAAGGTTG 900
Db 841 TGTGTGATCTTAACTAGTAGACGGAACCTAAGTCAATATCTCTCTTAAAGCAAAAGGTTG 900
QY 901 ATGAACCTTTGACCTTATTCGTGTGAGAAAAAATAAAAAA 943
Db 901 ATGAACCTTTGACCTTATTCGTGTGAGAAAAAATAAAAAA 943

RESULT 3
ADD30735
ID ADD30735 standard; cDNA; 943 BP.
XX
AC ADD30735;
XX
DT 15-JAN-2004 (first entry)
XX
DE Plant yield-related polynucleotide clone G1759.
XX
KW ds; transcription factor; transgenic plant; growth rate; senescence;
KW seed germination rate; plant vigor; seedling vigor.
XX
OS Arabidopsis thaliana.
XX
PN WO2003013227-A2.
XX
PD 20-FEB-2003.
XX
PP 09-AUG-2002; 2002WO-US025805.
XX
PR 09-AUG-2001; 2001US-0310847P.
PR 19-NOV-2001; 2001US-0336049P.
PR 11-DEC-2001; 2001US-0338692P.
PR 14-JUN-2002; 2002US-00171468.
XX
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
PI Ratcliffe O, Riechmann JL, Adam LJ, Dubell AT, Heard JE;
PI Pilgrim ML, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G;
PI Broun PS;
XX
DR WPI; 2003-248221/24.
DR P-PSDB; ADD30736.
XX
PT New plant transcription factor polynucleotides and polypeptides, useful
PT in producing transgenic plants with commercially valuable properties,
PT such as an alteration in a plant growth characteristic, e.g. growth rate
PT or apomixis.
XX
PS Disclosure; SEQ ID NO 764; 454pp; English.
XX
CC The invention relates to a number of isolated Arabidopsis thaliana cDNA
CC sequences and their encoded proteins which are especially transcription
CC factor related cDNA's and proteins. The isolated or recombinant plant
CC transcription factor polynucleotides and polypeptides are useful in
CC producing transgenic plants with commercially valuable properties, i.e.
CC modified or altered desirable traits as compared to a reference plant,
CC such as an alteration in a plant growth characteristic, e.g. growth rate,
CC germination rate of seeds, vigor of plants and seedlings, or leaf and
CC flower senescence. Sequence information related to the polynucleotides
CC and polypeptides can also be used in bioinformatic search methods. The
CC transgenic plant is useful for growing a progeny plant from a parent
CC plant. This sequence represents one of the cDNAs of the invention.
XX

SQ		Sequence 943 BP; 319 A; 193 C; 203 G; 228 T; 0 U; 0 Other;	
Query Match		100.0%; Score 943; DB 10; Length 943;	
Best Local Similarity		100.0%; Pred. No. 1.2e-240;	
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CGAGAAAGGAAAAAATAAGAGAGAAAAAGCTTAGTATCTCCGGCGACTTGAAC	60
Db	1	CGAGAAAGGAAAAAATAAGAGAGAAAAAGCTTAGTATCTCCGGCGACTTGAAC	60
Qy	61	CCAAACTGAGGATCAAAATTAGGGCAAAAGCCCTCTCGAGAGAGCCATGGAGAA	120
Db	61	CCAAACTGAGGATCAAAATTAGGGCAAAAGCCCTCTCGAGAGAGCCATGGAGAA	120
Qy	121	AAACTAGGAATCAAGCGAATTCGACACAAAGTAGCCGACAGTCACTTCTCCAAACG	180
Db	121	AAACTAGGAATCAAGCGAATTCGACACAAAGTAGCCGACAGTCACTTCTCCAAACG	180
Qy	181	TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTCTCTGTGAGCGCATCCGTCGC	240
Db	181	TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTCTCTGTGAGCGCATCCGTCGC	240
Qy	241	TCCTCTCGTCTCGCCCTCCGGCAAGCTCTACAGCTTCTCCGGCGAATACCTGGT	300
Db	241	TCCTCTCGTCTCGCCCTCCGGCAAGCTCTACAGCTTCTCCGGCGAATACCTGGT	300
Qy	301	CAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA	360
Db	301	CAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA	360
Qy	361	GTCAAAGCTCTGAATCTATGGTTCACTATGAGTACTTGAACCTTGTGATAGCAAGCT	420
Db	361	GTCAAAGCTCTGAATCTATGGTTCACTATGAGTACTTGAACCTTGTGATAGCAAGCT	420
Qy	421	TGTGGATCAAAATGTCAAAATGTGATATCGATCGATGCTTGTGTTCAACTGGAGGAAACCT	480
Db	421	TGTGGATCAAAATGTCAAAATGTGATATCGATCGATGCTTGTGTTCAACTGGAGGAAACCT	480
Qy	481	TGAGATCGCCCTCCGTGACTAGAGCCAGAGAGCCGACTCATCTGTGAGGCTTCTGA	540
Db	481	TGAGATCGCCCTCCGTGACTAGAGCCAGAGAGCCGACTCATCTGTGAGGCTTCTGA	540
Qy	541	GAATCTTAAAGAAAGGAGAAAAATGCTGAAAGAGAGAACCGATTTTGGCTAGCCAGAT	600
Db	541	GAATCTTAAAGAAAGGAGAAAAATGCTGAAAGAGAGAACCGATTTTGGCTAGCCAGAT	600
Qy	601	GGAGAAATATCATATGTGGGAGCAGAGCTGAGATGGAGATGTCACTGCTGGACAAAT	660
Db	601	GGAGAAATATCATATGTGGGAGCAGAGCTGAGATGGAGATGTCACTGCTGGACAAAT	660
Qy	661	CTCCGACAACTTCCGGTGAATCTCCCACTTAAATAGCCACCTTAAATCGCGGTTG	720
Db	661	CTCCGACAACTTCCGGTGAATCTCCCACTTAAATAGCCACCTTAAATCGCGGTTG	720
Qy	721	AAATCAAAATCCAAACATATATAATTAAGAAAAAATAAGATATGTAATTAT	780
Db	721	AAATCAAAATCCAAACATATATAATTAAGAAAAAATAAGATATGTAATTAT	780
Qy	781	CCGCTGATAGGGCGAGCGTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGCTTGG	840
Db	781	CCGCTGATAGGGCGAGCGTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGAGCTTGG	840
Qy	841	TGTGTACTTAAAGTAGCGGAACTAAGTCAATATCTGTTTAAAGCAAAAGGTTG	900
Db	841	TGTGTACTTAAAGTAGCGGAACTAAGTCAATATCTGTTTAAAGCAAAAGGTTG	900
Qy	901	ATGAACCTTGTACTTATTCGTGTGAGAAAAAATAAGAAAAA	943
Db	901	ATGAACCTTGTACTTATTCGTGTGAGAAAAAATAAGAAAAA	943

CC bioinformatic search methods. This sequence represents a plant
CC transcription factor, and an orthologue of Arabidopsis thaliana
CC transcription factors isolated in the invention, that can be used in the
CC creation of a transgenic plant with altered traits.

XX SQ Sequence 943 BP; 319 A; 193 C; 203 G; 228 T; 0 U; 0 Other;

Query Match 100.0%; Score 943; DB 12; Length 943;
Best Local Similarity 100.0%; Pred. No. 1.2e-240;
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAGAAAGGAAAAAATAAGAGAGAAAAAGCTTAGTATCTCGGCGACTTGAAC 60
Db 1 CGAGAAAGGAAAAAATAAGAGAGAAAAAGCTTAGTATCTCGGCGACTTGAAC 60

Qy 61 CCAAACTGAGGATCAAAATTAGGCGACAAGCCCTCTCGGAGAGAGCCATGGAGAAA 120
Db 61 CCAAACTGAGGATCAAAATTAGGCGACAAGCCCTCTCGGAGAGAGCCATGGAGAAA 120

Qy 121 AAAACTAGAAATCAAGCGAATTGAGAACAAAGTAGCGCAAGTCACTTCTCCAAACG 180
Db 121 AAAACTAGAAATCAAGCGAATTGAGAACAAAGTAGCGCAAGTCACTTCTCCAAACG 180

Qy 181 TCGCAACGGTCTCATCGAGAAAGCTCGTCAAGCTTCTGTTCTGTGACGATCCGTCGC 240
Db 181 TCGCAACGGTCTCATCGAGAAAGCTCGTCAAGCTTCTGTTCTGTGACGATCCGTCGC 240

Qy 241 TCTTCTCGTCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGCGGATACCTGGT 300
Db 241 TCTTCTCGTCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGCGGATACCTGGT 300

Qy 301 CAAGATCTTGATCGATATGGGAAACAGATGCTGTATGATCTTAAAGCCTTGGATATCA 360
Db 301 CAAGATCTTGATCGATATGGGAAACAGATGCTGTATGATCTTAAAGCCTTGGATATCA 360

Qy 361 GTCAAAAGCTCTGAATCTATGTTTCCACACTATGACTACTTGAATCTGTGATGACAGCT 420
Db 361 GTCAAAAGCTCTGAATCTATGTTTCCACACTATGACTACTTGAATCTGTGATGACAGCT 420

Qy 421 TGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTGTTCAACTGGAGGAACACT 480
Db 421 TGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTGTTCAACTGGAGGAACACT 480

Qy 481 TGAGACTGCCCTCTCCGTGATAGAGCAAGAGACCGAACTCATGTTGAGCTTGTGTA 540
Db 481 TGAGACTGCCCTCTCCGTGATAGAGCAAGAGACCGAACTCATGTTGAGCTTGTGTA 540

Qy 541 GAATCTTAAAGAAAGAGAGAAATGCTGAAGAGAGAACAGGTTTGGCTAGCCAGAT 600
Db 541 GAATCTTAAAGAAAGAGAGAAATGCTGAAGAGAGAACAGGTTTGGCTAGCCAGAT 600

Qy 601 GGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACTGCTGGACAAAT 660
Db 601 GGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACTGCTGGACAAAT 660

Qy 661 CTCGCAATCTTCCGGTGTACTCTCCCACTATTAATTAATGACCACTTAATTAATGAGCTTTG 720
Db 661 CTCGCAATCTTCCGGTGTACTCTCCCACTATTAATTAATGACCACTTAATTAATGAGCTTTG 720

Qy 721 AAATCAAAATCCAAACATATATTAATCAAGAAAAAATAAGATATGTAATTAAT 780
Db 721 AAATCAAAATCCAAACATATATTAATCAAGAAAAAATAAGATATGTAATTAAT 780

Qy 781 CCCTGATAGGGCGGCTTTGTATATCTTAATATCTCTCTTGTGGCCAAAGAGCTTTG 840
Db 781 CCCTGATAGGGCGGCTTTGTATATCTTAATATCTCTCTTGTGGCCAAAGAGCTTTG 840

Qy 841 TGTGTGATCTTAAGTAGACGGAACCTAAGTCAATATCTATCTGTTTAAAGCAAAAGCTTG 900
Db 841 TGTGTGATCTTAAGTAGACGGAACCTAAGTCAATATCTATCTGTTTAAAGCAAAAGCTTG 900

Qy 901 ATGAACCTTTGATCTTATTCGTGTGAGAAAAAATAAAAAA 943
|||||

Db 901 ATGAACCTTTGATCTTATTCGTGTGAGAAAAAATAAAAAA 943

RESULT 5
ADO03460
ID ADO03460 standard; cDNA; 943 BP.
XX ADO03460;
AC ADO03460;
XX
DT 01-JUL-2004 (first entry)
XX
DE Thalecress transcription factor cDNA #562.
KW Thalecress; transcription factor; ss; gene; plant; transgenic;
KW abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;
KW phosphate limitation; potassium limitation; nitrogen limitation;
KW hormone sensitivity; disease resistance; sugar sensing; seed germination;
KW flowering; inflorescence architectural change;
KW meristem cell differentiation; phyllotaxy; apical dominance;
KW trichome development; seed development; premature senescence;
KW delayed senescence; lethality; necrosis; plant size; leaf morphology;
KW seed morphology; secondary metabolism; light response; shade avoidance.

XX Arabidopsis thaliana.
XX
XX US2004045049-A1.
XX
XX 04-MAR-2004.
XX
XX 10-APR-2003; 2003US-00412699.
XX
XX 13-SEP-1999; 99US-00394519.
XX 21-JAN-2000; 2000US-00489376.
XX 17-FEB-2000; 2000US-00506720.
XX 22-MAR-2000; 2000US-00532591.
XX 22-MAR-2000; 2000US-00533029.
XX 22-MAR-2000; 2000US-00533030.
XX 22-MAR-2000; 2000US-00533392.
XX 22-MAR-2000; 2000US-00533648.
XX 06-APR-2000; 2000WO-US009448.
XX 16-NOV-2000; 2000US-00713994.
XX 27-MAR-2001; 2001US-00819142.
XX 17-APR-2001; 2001US-00837444.
XX 30-JAN-2002; 2002US-00958131.
XX 14-JUN-2002; 2002US-00171468.
XX 09-AUG-2002; 2002US-00225066.
XX 09-AUG-2002; 2002US-00225067.
XX 09-AUG-2002; 2002US-00225068.
XX 17-DEC-2002; 2002US-0434166P.
XX 25-FEB-2003; 2003US-00374780.

(ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.

XX Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE;
PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS;
PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;

OS Arabidopsis thaliana.

XX Key Location/Qualifiers
 XX CDS 1..591
 XX /*tag= a
 XX /product= "FLC1"
 XX /note= "Flowering locus C 1 protein"

XX WO200050615-A1.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US004940.

XX 25-FEB-1999; 99US-0121572P.

XX 09-MAR-1999; 99US-0123455P.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX Amasino RM, Schomburg PM, Michaels SD, Sung S, Scortecci K;

XX P-PSDB; AAY94703.

XX WPI; 2000-533182/48.

XX member of the flowering locus C gene family in its genome.
 XX New transgenic plant with altered flowering time has a transgene for a

XX Claim 12; Page 36-37; 56pp; English.

XX This invention relates to a transgenic plant that comprises in its genome
 CC a transgene encoding a member of the flowering locus C (FLC) gene family.
 CC The transgenic plant has an altered timing of its flowering time compared
 CC to non-transgenic plants of the same species. The invention includes a
 CC seed of the transgenic plant which contains a plant expressible promoter
 CC and a protein coding region for a plant FLC protein which has a MADS box
 CC domain, and is effective at causing a delay in flowering time when
 CC expressed in a plant. FLC genes are MADS box genes. The MADS box is a
 CC highly conserved motif shared by a group of transcription factors. The
 CC methods of the invention are used to produce transgenic plants with
 CC altered flowering characteristics compared to flowering plants of the
 CC same species. Altering the flowering time allows the vegetative growth or
 CC flower creation by a plant to be increased, depending on the type of
 CC plant and the needs of the plant breeder. Transgenic plants which can be
 CC produced include monocotyledons e.g. asparagus, onions, maize, barley and
 CC turf grasses and dicotyledonous plants e.g. tomato, beans, cotton,
 CC flowers and shrubs. The methods disclosed in the invention allow the
 CC flowering time of the transgenic plant to be altered in either direction
 CC when compared to the wild-type plant. The present sequence represents
 CC Arabidopsis thaliana cDNA encoding the FLC1 protein. The cDNA and protein
 CC sequences are used in the construction of the transgenic plant of the
 CC invention

XX SQ Sequence 797 BP; 261 A; 167 C; 169 G; 200 T; 0 U; 0 Other;

XX Query Match 83.2%; Score 784.4; DB 3; Length 797;

XX Best Local Similarity 99.9%; Pred. No. 2.1e-198;

XX Matches 785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 110 ATGGGAGAGAAAACTAGAAATCAAGCAATTCAGAACAAAGTAGCCGCAAGTCACC 169

XX 1 ATGGGAGAGAAAACTAGAAATCAAGCAATTCAGAACAAAGTAGCCGCAAGTCACC 60

XX 170 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGAC 229

XX 61 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGAC 120

XX 230 GCATCCGTCGCTCTTCTCGTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCGGC 289

XX 121 GCATCCGTCGCTCTTCTCGTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCGGC 180

XX 290 GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCC 349

XX 181 GATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCC 240

QY 350 TTGGATCATAGTCAAAAAGCTCTGAACTATAGTTCACTAGAGCTACTTGAACCTTGTG 409
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 DB 241 TTGGATCATAGTCAAAAAGCTCTGAACTATAGTTCACTAGAGCTACTTGAACCTTGTG 300
 QY 410 GATAGCAAGCTTTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCACATG 469
 DB |||||
 DB 301 GATAGCAAGCTTTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTTCACATG 360
 QY 470 GAGGAACACCTTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAACACGAACTCAATGTTG 529
 DB |||||
 DB 361 GAGGAACACCTTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAACACGAACTCAATGTTG 420
 QY 530 AAGCTTTGTGAGAAATCTTAAAGAAAGGAGAAAAATGCTGAAAGAGAGAACCAAGGTTTGTG 589
 DB |||||
 DB 421 AAGCTTTGTGAGAAATCTTAAAGAAAGGAGAAAAATGCTGAAAGAGAGAACCAAGGTTTGTG 480
 QY 590 GCTAGCCAGATGGAGAAATCAATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCT 649
 DB |||||
 DB 481 GCTAGCCAGATGGAGAAATCAATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCT 540
 QY 650 GCTGACAAATCTCCGACAAATCTTCCGGTGACTCTCCCACTACTTAAATTAGCCACCTTAA 709
 DB |||||
 DB 541 GCTGACAAATCTCCGACAAATCTTCCGGTGACTCTCCCACTACTTAAATTAGCCACCTTAA 600
 QY 710 ATCGCGGTTGAAATCAAAATCCAAATCATATATAATTAATGAGAAAAAATAAGAT 769
 DB |||||
 DB 601 ATCGCGGTTGAAATCAAAATCCAAATCATATATAATTAATGAGAAAAAATAAGAT 660
 QY 770 ATGTAATTTATCCCGCTGATAGGGCGGAGCGTTTGTATATCTTAATACTCTCTCTTTGGCC 829
 DB |||||
 DB 661 ATGTAATTTATCCCGCTGATAGGGCGGAGCGTTTGTATATCTTAATACTCTCTCTTTGGCC 720
 QY 830 AAGAGACTTTGTGTGTGATCTTAAGTAGAGCGAACTAAGTCAATACTATCTGTTTTAAG 889
 DB |||||
 DB 721 AAGAGACTTTGTGTGTGATCTTAAGTAGAGCGAACTAAGTCAATACTATCTGTTTTAAG 780
 QY 890 AAAAA 895
 DB |||||
 DB 781 AAAAA 786

RESULT 7
 AAC39385
 ID AAC39385 standard; DNA; 758 BP.
 AC AAC39385;
 XX AAC39385;
 DT 17-OCT-2000 (first entry)
 XX
 XX Arabidopsis thaliana DNA fragment SEQ ID NO: 24438.
 XX
 XX Hybridisation assay; genetic mapping; gene expression control;
 XX protein identification; signal transduction pathway; metabolic pathway;
 XX promoter; termination sequence; ss.
 XX Arabidopsis thaliana.
 XX EP1033405-A2.
 XX PD 06-SEP-2000.
 XX
 XX 25-FEB-2000; 2000EP-00301439.
 XX
 XX 25-FEB-1999; 99US-0121825P.
 XX 03-MAR-1999; 99US-0123180P.
 XX 09-MAR-1999; 99US-0123548P.
 XX 23-MAR-1999; 99US-0125788P.
 XX 25-MAR-1999; 99US-0126264P.
 XX 29-MAR-1999; 99US-0126785P.
 XX 01-APR-1999; 99US-0127462P.
 XX 08-APR-1999; 99US-0128234P.
 XX 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.
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PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
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PR 24-MAY-1999; 99US-0135829P.
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PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
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PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
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PR 04-OCT-1999; 99US-0157117P.
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PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.

QY 350 TTGATCATCAGTCAAAAGCTCTGAACATATGGTTTCACTATGAGCTACTTGAACCTGTG 409
Db 241 TTGATCATCAGTCAAAAGCTCTGAACATATGGTTTCACTATGAGCTACTTGAACCTGTG 300
QY 410 GATAGCAAGCTTGGGATCAAAATGTCAAAATGTCAGTATGATGCTCTTGTTCAACTG 469
Db 301 GATAGCAAGCTTGGGATCAAAATGTCAAAATGTCAGTATGATGCTCTTGTTCAACTG 360
QY 470 GAGGACACCTTGAGACTGCCCTCCGTCAGCTAGAGCCCAAGAGACCGAATCATGTTG 529
Db 361 GAGGACACCTTGAGACTGCCCTCCGTCAGCTAGAGCCCAAGAGACCGAATCATGTTG 420
QY 530 AAGCTTGTTCAGAAATCTTAAAGAAAAGGAGAAAATGCTGAAAAGAGAACACCGGTTTGG 589
Db 421 AAGCTTGTTCAGAAATCTTAAAGAAAAGGAGAAAATGCTGAAAAGAGAACACCGGTTTGG 480
QY 590 GCTAGCCAGATGAGAAATATCATGTCGAGGAGGAGAACCTGAGATGGAGATGTCACT 649
Db 481 GCTAGCCAGATGAGAAATATCATGTCGAGGAGGAGAACCTGAGATGGAGATGTCACT 540
QY 650 GCTGGCAAAATCTCCGACATCTTCCGGTGAATCTCCCACTACTTAATTAG 700
Db 541 GCTGGCAAAATCTCCGACATCTTCCGGTGAATCTCCCACTACTTAATTAG 591

RESULT 9

AAA29035
ID AAA29035 standard; cDNA; 868 BP.
XX AC AAA29035;
DT 12-SEP-2000 (first entry)
XX DE B. napus flowering locus F (PLF) homologous cDNA 4.
XX KW Flowering locus F; transcription factor; DNA binding domain; MADS box;
XX KM PLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
XX OS Brassica napus.
XX FH Key Location/Qualifiers
XX FT CDS 80..673
XX FT /*tag= a
XX FT /product= "PLF_homologue"
XX PN WO200032780-A1.
XX PD 08-JUN-2000.
XX PF 02-DEC-1999; 99WO-AU001079.
XX PF 03-DEC-1998; 98AU-00007469.
XX PR 22-JAN-1999; 99US-0116928P.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (PERE/) PEREZ P.
XX Perez P, Burn JE, Peacock WJ, Dennis ES, Sheldon CC;
PI Helliwell CA, Rouse DT;
XX WPI; 2000-451762/39.
DR P-PSDB; AAY96411.
XX New nucleic acid comprising a MADS box that encodes a transcription
PT factor for altering the flowering time or modifying the vegetative or
PT floral phenotype of a plant such as wheat.
XX Claim 6; Page 87-88; 106pp; English.
XX AAA29032-41 are cDNA clones isolated from a Brassica napus cDNA library
CC using hybridisation to an PLF (flowering locus F) cDNA from Arabidopsis
CC thaliana. From both amino acid and nucleotide sequence data it was
CC concluded that the clones represent transcripts from 5 different genes.

The PLF gene encodes a transcription factor protein comprising a distinctive conserved DNA binding domain (a MADS box). The DNA was identified from a late-flowering mutant (flf), which arose during transformation of the early-flowering ecotype C24 with a modified binary vector pBin-delta-Ac. It was found that two T-DNAs segregate in the very late flowering phenotype and that two expressed genes (A and B) were closely linked to these T-DNAs. Gene B was re-designated as PLF. The PLF gene is linked to the top of chromosome 5, 4 cm from RFLP marker 447. The protein is capable of altering the flowering time of a plant. Over-expression of the PLF gene can be used to delay flowering in a plant. Alternatively, reduction of PLF gene expression, e.g. by antisense constructs, can be used to induce early flowering. Methods of modifying the level of expression of a PLF gene to modify the production or activity of a gibberellin in the plant are also claimed. The response of a plant to vernalization can also be altered. Any dicotyledonous or monocotyledonous plant species including horticultural plants, particularly those in the cut-flower industry, vegetable, cereal and other crop plants are capable of being controlled

Sequence 868 BP; 273 A; 187 C; 196 G; 212 T; 0 U; 0 Other;

Query Match 57.1%; Score 538.4; DB 3; Length 868;
Best Local Similarity 81.7%; Pred. No. 7.4e-133;
Matches 688; Conservative 0; Mismatches 136; Indels 18; Gaps 5;

QY 33 AAGCTTAGTATCTCGGCGACTTGAACCCAACTGAGGATCAATATTAGGCACAAAGC 92
Db 1 AAGCTTCAGTATCTCGGCTAGTGGAAACCGGACCTCAAGATCAATATTAGGCGCAAGC 60
QY 93 CCTCTCGGAG--AGAAGCCATGGAGAAAGAACTAGAAATCAAGCGAATTCGAGAACAA 150
Db 61 ACTGTTGGAGACAGAACCCATCGGGAGGAGAACTTGAATTCAGCGAATTCGAGAACAA 120
QY 151 AAGTAGCCGACAAAGTCACCTTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCA 210
Db 121 AAGTAGCCGACAAAGTTACCTTCTTAACGACGCAACGGTCTCATCGAGAAAGCTCGTCA 180
QY 211 GCTTTCTGTTCTCTGTGACGCATCCGTCGCTCTTCTCGTCGTCCTCCGCTCCGGCAGCT 270
Db 181 GCTTTCCGTTCTCTGTGACGCATCCGTCGCTCTTCTGTGCTCTCCGCTCCGGGAAACT 240
QY 271 CTACAGCTTCTCTCCGCGGATAAACCCTGGTCAAGATCCTTGATCGATATGGGAAACAGCA 330
Db 241 CTACAGCTTCTCTCCGCTGATTAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCA 300
QY 331 TGCTGATGATCTTAAAGCCCTTGATCATCAGTCAAAAGCTCTGAACTATGTTTCACACTA 390
Db 301 TGATGATGATCTTAAAGCCCTTGATCGTCAAGCTTAAAGGCTTTGGAGCTGTGTTTCACACCA 360
QY 391 TGAGCTACTTGAACCTTGGATAGCAAGCTTCTGGGATCAATATGTCAAAATCTGAGTAT 450
Db 361 TGAGCTACTTGAACCTTGGGAAAGCAAGCTTGAGGAATCAATATGTCGATTAATGTAAGTGT 420
QY 451 CGATGCTCTTGTTCAACTCGGAGAACACCTTCAGACTGCGCTCTCCGTCAGCTAGAGCCAA 510
Db 421 GGGTTCCTCGTTTTCAGCTGGAGAACACCTTCGAGAACGCCCTCTCCGTAACAGAGCTAG 480
QY 511 GAAGACCGAATCTCATGTTGAAGCTTGTTCAGAACTCTTAAAGAAAGAGAGAAATGCTGAA 570
Db 481 GAAGACAGAACTAAATGTTGAAGCTTGTTCAGAACTCTTAAAGAAAGAGAGAAATGCTGGA 540
QY 571 AGAAGAGAACAGGTTTGGCTAGCAGATGAGAAATATCATGTCGAGGAGCAGAACG 630
Db 541 AGAGAGAACCCATGTTTGGCTAGCAGATGAGAAAGAGTAAATCTTGTGCGAGCCGAGC 600
QY 631 TGAGATGGAGATGTCACTGCTGGCAAAATCTCCGA---CAATCTTCCGGTGAATCTCCC 687
Db 601 TGATTAATGATGATGTCTACAGGAGCAATCTCCGACATCAATCTTCCGTAACGCTCCC 660
QY 688 ACTACTTAATTAGCACCTTAAATCGCGGTTGAAATCAAAATCCAAAACATATATAATT 747
Db 661 ACTGCTTAATTAGTCACTTTAAATCGGCAAT--AAATAAAATCCAAAACATAT----- 712

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XX	DB	1	TCGGGCTAGTGGNAACCGGACCTCAAGATCAAAATTAGGGCGCAAGCATGTTGGAGACA	60
XX	QY	104	GAAGCCATGGGAAGAAAAAACTAGAAATCAAGCGAATTGAGAACAAAAAGTAGCCGACAA	163
XX	DB	61	GAAGCCATGGGAGGAAGAAACTTGAATCAAGCGAATTGAGAACAAAAAGTAGCCGACAA	120
XX	QY	164	GTACACCTTCCAAAGCTGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTTCTC	223
XX	DB	121	GTACACCTTCTTAAACGACGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTTCTC	180
XX	QY	224	TGTGACGATCCGTGCTCTTCTGTCGCTCTCCGCTCCGCGAAGCTCTACAGCTTCTCC	283
XX	DB	181	TGTGACGATCCGTGCTCTTCTGTCGCTCTCCGCTCCGCGAAGCTCTACAGCTTCTCC	240
XX	QY	284	TCGGGCGATAACCTGGTCAAGATCCCTTGATCGATATGGGAAACAGCATGCTGATGATCT	343
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XX	QY	344	AAAGCCTTGGATCATCAAGCTCAAAAGCTCTGAAGTATGGTTCACACTATGAGCTACTTGA	403
XX	DB	301	AAAGCCTTGGATCATCAAGCTCAAAAGCTCTGAAGTATGGTTCACACTATGAGCTACTTGA	360
XX	QY	404	CTTGTGGATAGCAAGCTTGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTTGTGT	463
XX	DB	361	CTTGTGGATAGCAAGCTTGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTTGTGT	420
XX	QY	464	CAACTGGAGGAACAACCTTGAGATCCCTCTCCGTGACTAGAGCCAGAACGACCACTC	523
XX	DB	421	CAGCTGGAGGAACAACCTTGAGATCCCTCTCCGTGACTAGAGCCAGAACGACCACTC	480
XX	QY	524	ATGTTGAGATCTTGTGAGATCTTAAAGAAAGGAGGAAATCTGTAAGAGAGAACCCAG	583
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XX	QY	584	GTGTTGGCTAGCCAGATGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATG	643
XX	DB	541	GTGTTGGCTAGCCAGATGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGGAGATG	600
XX	QY	644	TCACCTGCTGGACAAATCTCCGA---CAATCTCCGGTGAATCTCCACTACTTAATAG	700
XX	DB	601	GTCTCACCAAGGACAAATCTCCGACATCAATCTCCGTAACGCTCCCACTGCTTAATAG	660
XX	QY	701	CCACTTAAATCGGCGGTGAATCAAAATCCAAACATATATATATGAAGAAAAA	760
XX	DB	661	TCACCTTAAATCGGCGGTGAATCAAAATCCAAACATATATATATGAAGAAAAA	708
XX	QY	761	AAATAAGATATGTAATTAATTCGCTGATAAGGCGAGCGTTTGTATATCTTAATCTCTC	820
XX	DB	709	AAACAAGATGTAATTAATTCGCTGATAAGGCGGTGACGTTGTATATCTTACTCTCTC	768
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XX	DB	769	TC-CGGCTCGAGAGGCTCGGGGTGTAAGAACTATTTCAGATTTATGTGAAG	816
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XX	AC	AAA29034;		
XX	DT	12-SEP-2000	(first entry)	
XX	DE	B. napus	flowering locus F (FLF) homologous cDNA 3.	
XX	KW	Flowering locus F;	transcription factor; DNA binding domain; MADS box;	
XX	KW	FLF; chromosome 5;	RFLP marker 447; flowering time; vernalization; ss.	
XX	OS	Brassica napus.		
XX	FX	Key	Location/Qualifiers	
XX	FX	CDS	67..660	
XX	FX	FT	/*tag= a	
XX	FX	PN	/product= "FLF_homologue"	
XX	PD	WO200032780-A1.		
XX	PD	08-JUN-2000.		
XX	PF	02-DEC-1999;	99WO-AU001079.	
XX	PR	03-DEC-1998;	98AU-00007469.	
XX	PR	22-JAN-1999;	99US-0116928P.	
XX	PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.		
XX	PA	(PERE/) PEREZ P.		
XX	PI	Perez P, Burn JE, Peacock WJ, Dennis ES, Sheldon CC;		
XX	PI	Helliwell CA, Rouse DT;		
XX	XX	WPI; 2000-451762/39.		
XX	DR	P-PSDB; AAY96417.		
XX	PT	New nucleic acid comprising a MADS box that encodes a transcription		
XX	PT	factor for altering the flowering time or modifying the vegetative or		
XX	PT	floral phenotype of a plant such as wheat.		
XX	PS	Claim 6; Page 90-91; 106pp; English.		
XX	CC	AAA29032-41 are cDNA clones isolated from a Brassica napus cDNA library		
XX	CC	using hybridisation to an FLF (flowering locus F) cDNA from Arabidopsis		
XX	CC	thaliana. From both amino acid and nucleotide sequence data it was		
XX	CC	concluded that the clones represent transcripts from 5 different genes.		
XX	CC	The FLF gene encodes a transcription factor protein comprising a		
XX	CC	distinctive conserved DNA binding domain (a MADS box). The DNA was		
XX	CC	identified from a late-flowering mutant (elf), which arose during		
XX	CC	transformation of the early-flowering ecotype C24 with a modified binary		
XX	CC	vector pBin-delta-Ac. It was found that two T-DNAs segregate in the very		
XX	CC	late flowering phenotype and that two expressed genes (A and B) were		
XX	CC	closely linked to these T-DNAs. Gene B was re-designated as FLF. The FLF		
XX	CC	gene is linked to the top of chromosome 5, 4 cm from RFLP marker 447. The		
XX	CC	protein is capable of altering the flowering time of a plant. Over-		
XX	CC	expression of the FLF gene can be used to delay flowering in a plant.		
XX	CC	Alternatively, reduction of FLF gene expression, e.g. by antisense		
XX	CC	constructs, can be used to induce early flowering. Methods of modifying		
XX	CC	vegetative and/or floral phenotypes of a plant comprising increasing the		
XX	CC	level of expression of a FLF gene to modify the production or activity of		
XX	CC	a gibberellin in the plant are also claimed. The response of a plant to		
XX	CC	vernalization can also be altered. Any dicotyledonous or monocotyledonous		
XX	CC	plant species including horticultural plants, particularly those in the		
XX	CC	cut-flower industry, vegetable, cereal and other crop plants are capable		
XX	CC	of being controlled		
XX	SQ	Sequence 891 BP; 276 A; 191 C; 202 G; 222 T; 0 U; 0 Other;		
XX	Query Match	55.9%; Score 527; DB 3; Length 891;		
XX	Best Local Similarity	81.5%; Pred. No. 8.2e-130;		
XX	Matches	676; Conservative 0; Mismatches 135; Indels 18; Gaps 5;		

CDS 46..639
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 /product= "FLF_homologue"
 WO200032780-A1.
 08-JUN-2000.
 02-DEC-1999; 99WO-AU001079.
 03-DEC-1998; 98AU-00007469.
 22-JAN-1999; 99US-0116928P.
 (CSIR) COMMONWEALTH SCI & IND RES ORG.
 (PERE/) PEREZ P.
 Perez P, Burn JE, Peacock WJ, Dennis ES, Sheldon CC;
 Helliwell CA, Rouse DT;
 WPI; 2000-451762/39.
 P-PSDB; AAY96410.
 New nucleic acid comprising a MADS box that encodes a transcription
 factor for altering the flowering time or modifying the vegetative or
 floral phenotype of a plant such as wheat.
 Claim 6; Page 87; 106pp; English.
 AAA29032-41 are cDNA clones isolated from a Brassica napus cDNA library
 using hybridisation to an FLF (flowering locus P) cDNA from Arabidopsis
 thaliana. From both amino acid and nucleotide sequence data it was
 concluded that the clones represent transcripts from 5 different genes.
 The FLF gene encodes a transcription factor protein comprising a
 distinctive conserved DNA binding domain (a MADS box). The DNA was
 identified from a late-flowering mutant (flf), which arose during
 transformation of the early-flowering ecotype C24 with a modified binary
 vector pbin-delta-3c. It was found that two T-DNAs segregate in the very
 late flowering phenotype and that two expressed genes (A and B) were
 closely linked to these T-DNAs. Gene B was re-designated as FLF. The FLF
 gene is linked to the top of chromosome 5, 4 cm from RFLP marker 447. The
 protein is capable of altering the flowering time of a plant. Over-
 expression of the FLF gene can be used to delay flowering in a plant.
 Alternatively, reduction of FLF gene expression, e.g. by antisense
 constructs, can be used to induce early flowering. Methods of modifying
 vegetative and/or floral phenotypes of a plant comprising increasing the
 level of expression of a FLF gene to modify the production or activity of
 a gibberellin in the plant are also claimed. The response of a plant to
 vernalization can also be altered. Any dicotyledonous or monocotyledonous
 plant species including horticultural plants, particularly those in the
 cut-flower industry, vegetable, cereal and other crop plants are capable
 of being controlled
 SQ Sequence 969 BP; 281 A; 206 C; 218 G; 264 T; 0 U; 0 Other;
 Query Match 52.58; Score 494.8; DB 3; Length 969;
 Best Local Similarity 80.6%; Pred. No. 3.2e-121;
 Matches 656; Conservative 0; Mismatches 142; Indels 16; Gaps 6;
 67 CTGAGGATCAAAATTAGGGACAAAGCCCTCTCGGAG--AGAAGCCATGGGAGAGAAAAA 124
 1 CTCTGGATCAAAATTAGGGACAGAGACCACTTGGAGACAGAAACCACTTGGGAGAAAAA 60
 125 CTAGAAATCAAGCGAATTGAGAAACAAAGTAGCGCAACAGTCACCTTCTCCAAACGTCGC 184
 61 CTAGAAATCAAGCGAATTGAGAAACAAAGTAGCGCAACAGTCACCTTCTCCAAACGTCGC 120
 185 AAGGCTCTCATCGAGAAAGCTCGTCAGCTTCTGTTTCTCTGTGACGATCCGTCGCTTT 244
 121 AGCGGTCTCATTTGAGAAAGCTCGTCAGCTTCTGTTTCTCTGCGATGATCCGTCGCGCTT 180
 245 CTGCTGCTCTCCGCTCCGCGACAGCTCTACAGCTTCTCTCCGCGATACCTGCTCAAG 304
 181 CTGTTGCTCTCTCTCCGCGACAGCTCTACAGCTTCTCTCCGCGGTGATAACCTGGTCAGG 240

QY 305 ATCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTTGGATCATCAGTCA 364
 DB 241 ATCTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTTGGATCATCAGTCA 300
 QY 365 AAGCTCTGAACTATGTTTCACTATGAGCTACTTGAACCTTGGATGAGCAAGCTTGTG 424
 DB 301 AAGCTCTGAGCTATGTTTCACTATGAGCTACTTGAACCTTGGATGAGCAAGCTTGTG 360
 QY 425 GGATCAAAATGTCAAAAATGTGAGTATCGATGCTTCTGTTCAACTGGAGGAGACACTTTCAG 484
 DB 361 GAATCAAAATGTGAGTATCGATGCTTCTGTTCAACTGGAGGAGACACTTTCAG 420
 QY 485 ACTGCCCTCTCCGTTGACTAGAGCAAGACCGAACTCATGTTGAGAGCTTGTGAGAAAT 544
 DB 421 AATGCCCTCTCTCTAACTAGAGCTAGGAGACAGAACTAATGTTGAAGCTTGTGATAGC 480
 QY 545 CTTAAGAGAAAGGAGAAATGCTGAAAGAGAGAGAACAGGTTTGGCTAGCCAGATGGAG 604
 DB 481 CTCAAGAGAAAGGAGAAAGCTGCTGAAGAGAGAGAAATCAGGCTTTGGCTGGCCAGAGGAG 540
 QY 605 AATAATCATCATGTGGGAGCAGAGCTGAGATGTCACCTGTGAGCAAAATCTCC 664
 DB 541 AAGAGAGATCTTGGGAGCGGAGCTGATATATGAGAGATGTCACCTGTGAGCAAAATCTCC 600
 QY 665 GA---CAATCTCCGGTGAATCTCCCACTACTTAAATTTAGCCACCTTAAATCGGCGTTGA 721
 DB 601 GACATCAATCTCCGGTGAATCTCCCACTACTTAAATTTAGCCACCTTAAATCGGCGTTGA 657
 QY 722 AATCAAAATCAAAACATATATATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
 DB 658 GATCAAAATTAAG 713
 QY 782 CGCTGATAAGGGGAGGCTTGTGATATCTTAAATCTCTCTCTTTGGCCAGAGAGAGAGAG 841
 DB 714 ACCTTGAAGGGTGCAGG-TTGATATCTCATATCTC---CCTTGGCTGAGAGATGTTGT 769
 QY 842 GTGTGATACTTAAGTAGAGCGGAACCTAAGTCAATA 875
 DB 770 GTTACTCTCTATGTTAGATATATGAGTAAATA 803
 RESULT 13
 ADW76669
 ID ADW76669 standard; cDNA; 851 BP.
 XX
 AC ADW76669;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Chinese cabbage BcpFLC3 cDNA.
 XX
 KW BcpFLC3; ss; gene; flowering; plant.
 XX
 OS Brassica rapa subsp. pekinensis.
 XX
 FH Key Location/Qualifiers
 FT CDS 55..648
 FT /*tag= a
 FT /product= "BcpFLC3 protein"
 FT /note= "this CDS, minus the stop codon, is specifically
 FT claimed in claim 1"
 XX
 XX CN1472320-A.
 XX
 XX 04-FEB-2004.
 PD
 XX 16-MAY-2003; 2003CN-00116982.
 XX
 XX 16-MAY-2003; 2003CN-00116982.
 PR
 XX (UYSH-) UNIV SHANGHAI COMMUNICATION.
 XX
 XX

PI Tang K, Li Z, Zhao L;
XX WPI; 2004-317408/30.
XX P-PSDB; ADW76670.
XX Chinese cabbage BcpFLC3 protein encoding array.
PT
XX
PS Claim 1; SEQ ID NO 1; 18pp; Chinese.
XX
CC The invention relates to the coding sequence of the Chinese cabbage
CC BcpFLC3 protein, which can suppress the bolting (?) or delay blossoming
CC (flowering). The present sequence encodes the BcpFLC3 protein. NOTE: The
CC specification has two sequence listings and consequently 2 different SEQ
CC ID 1 and SEQ ID 2. The present sequence is referred to as SEQ ID 3 in the
CC claims (which it would be since it follows after SEQ ID 2 of the first
CC sequence listing).
XX
SQ Sequence 851 BP; 272 A; 180 C; 189 G; 210 T; 0 U; 0 Other;

Query Match 52.2%; Score 491.8; DB 13; Length 851;
Best Local Similarity 80.1%; Pred. No. 1.9e-120;
Matches 656; Conservative 0; Mismatches 147; Indels 16; Gaps 6;

QY 62 CAACCTGAGGATCAATAGGCGACAAAGCCCTCTCGGAG--AGAAGCCATGGGAAGAA 119
Db |||||
QY 5 CTAGACTCTGGATCAAAATTAGGCGACAGAGACCCTTGGAGACAGAAACCATGGGAAGAA 64
Db |||||
QY 120 AAAAACTAGAAATCAAGCGAATTTGAGACAAAGTAGCCGACAGTCACCTTCTCCAAAC 179
Db |||||
QY 65 AAAAACTAGAAATCAAGCGAATTTGAGACAAAGTAGCCGACAGTCACCTTCTCCAAAC 124
Db |||||
QY 180 GTCCGACCGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGACGATCGTCG 239
Db |||||
QY 125 GACGACGCGTCTCATGAGAAAGCTCGTCAGCTTTCTGTTCTCTGCGATGCATCGTCG 184
Db |||||
QY 240 CTCTTCTCGTGTCTCGGCTCGGCAAGCTCTACAGCTTCTCTCCGCGGATAACCTGG 299
Db |||||
QY 185 CGCTTCTCGTGTCTCGGCTCGGCAAGCTCTACAGCTTCTCTCCGCGGATAACCTGG 244
Db |||||
QY 300 TCAAGATCCTTGATCGATATGGGAACAGCATGCTGATGATCTTAAGCCTTGGATCATC 359
Db |||||
QY 245 TCAGGATCCTTGATCGATATGGGAACAGCATGCTGATGATCTTAAGCCTTGGATCATC 304
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QY 605 TCTCCGACATCAATCTTCCGGTAATCTCCCACTACTTAATGAGCAGCTTGAAGCGGG 664
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QY 717 GTTGAATCAAAATCCAAACATATATATATATGAGAAAGAAAGAAATATGATATGTAAT 776
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QY 665 CT---GATCAATTAAGAAATCCAAACAT---ACAACTAATTAATTAAGCTTTGTTGT 717
Db |||||
QY 777 TATTCGCTGATAAGGCGAGGCTTTGTAATATCTTAATTAATCTCTCTTTTGGCCAGAGAC 836
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AC AAA29040;
XX
DT 12-SEP-2000 (first entry)
XX
DE B. napus flowering locus F (FLF) homologous cDNA 9.
XX
KW Flowering locus F; transcription factor; DNA binding domain; MADS box;
KW FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.
OS Brassica napus.
FH Key Location/Qualifiers
FT CDS 67..657
FT /*tag= a
FT /product= "FLF_homologue"
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PN WO200032780-A1.
XX
PD 08-JUN-2000.
XX
PP 02-DEC-1999; 99WO-AU001079.
XX
XX 03-DEC-1999; 99AU-00007469.
PR 22-JAN-1999; 99US-0116928P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (PERE/) PEREZ P.
XX
PI Perez P, Burn JE, Peacock WJ, Dennis ES, Sheldon CC;
PI Helliwell CA, Rouse DT;
XX
WPI; 2000-451762/39.
P-PSDB; AA96416.
PT New nucleic acid comprising a MADS box that encodes a transcription
PT factor for altering the flowering time or modifying the vegetative or
PT floral phenotype of a plant such as wheat.
PS Claim 6; Page 90; 106pp; English.
XX
CC AA29032-41 are cDNA clones isolated from a Brassica napus cDNA library
CC using hybridisation to an FLF (flowering locus F) cDNA from Arabidopsis
CC thaliana. From both amino acid and nucleotide sequence data it was
CC concluded that the clones represent transcripts from 5 different genes.
CC The FLF gene encodes a transcription factor protein comprising a
CC distinctive conserved DNA binding domain (a MADS box). The DNA was
CC identified from a late-flowering mutant (flf), which arose during
CC transformation of the early-flowering ecotype C24 with a modified binary
CC vector pBin-delta-Ac. It was found that two T-DNAs segregate in the very
CC late flowering phenotype and that two expressed genes (A and B) were
CC closely linked to these T-DNAs. Gene B was re-designated as FLF. The FLF
CC gene is linked to the top of chromosome 5, 4 cm from RFLP marker 447. The
CC protein is capable of altering the flowering time of a plant. Over-
CC expression of the FLF gene can be used to delay flowering in a plant.
CC Alternatively, reduction of FLF gene expression, e.g. by antisense
CC constructs, can be used to induce early flowering. Methods of modifying
CC vegetative and/or floral phenotypes of a plant comprising increasing the
CC level of expression of a FLF gene to modify the production or activity of
CC a gibberellin in the plant are also claimed. The response of a plant to
CC vernalization can also be altered. Any dicotyledonous or monocotyledonous
CC plant species including horticultural plants, particularly those in the
CC cut-flower industry, vegetable, cereal and other crop plants are capable

CC	of being controlled	
XX		
SQ	Sequence 825 BP; 265 A; 180 C; 181 G; 199 T; 0 U; 0 Other;	
Query Match		
Best Local Similarity 52.0%; Score 490.8; DB 3; Length 825;		
Matches 587; Conservative 0; Mismatches 97; Indels 8; Gaps 3;		
Qy	50 CGGACTTGAAACCCAAACCTGAGGATCAAAATAGGGCAAAAGCCCTCTCGAG--AGAAG 107	
Db	5 GAGAGTTGAAACCCGAATCTCAGGATCAAAATAGGGCAAAAGGCTTCTCGGAGACAGAAG 64	
Qy	108 CCATGGGAAGAAAGAAATAGAAATCAAGCGAATTGCAACAAAGTAGCGCAAGTCA 167	
Db	65 CCATGGGAAGAAAGAAATAGAGATCAAGCGAATTGAGAACAAAGTAGCGCAAGTCA 124	
Qy	168 CTTTCTCCAAACGTCGCAACGCTCTCATCGAGAAAGCTCGTCAGCTTTCTCTCTGTG 227	
Db	125 CTTTCTCCAAACGAGCAATGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTCTGTG 184	
Qy	228 ACGATCCGTCGCTCTTCTCGTGTCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCG 287	
Db	185 ATGATCCGTCGCTCTTCTCGTGTCTCAGCTCCGCAAGCTTTACAACCTTCTCCGCG 244	
Qy	288 GCGATAACCTGCTCAAGATCCTTGATGATATGGAAACAGCATGCTGATCTTAAAG 347	
Db	245 GCGATAACCTGCTCAAGATCCTTGATGATATGGAAACAAACATGCTGATCTTAAAG 304	
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Db	305 CTCTGGATCTTCACTCAAAAGCTCCGAAGTATGGTTCAACCATGAGCTACTAGAGTTG 364	
Qy	408 TGGATAGCAAGCTTGTGGATCAAAATGTCAAAAATGTGAGTATCGATCTCTTGTCAAC 467	
Db	365 TCGAAGTAAAGCTTGTGGAATCAAAAT--TCTGATGTAAGCGTCCGACTCCCTCGTTCAGC 421	
Qy	468 TGGAGGAACCTTGAGACTGCCCTCTCCGTCATGAGCCCAAGACCACTCATGT 527	
Db	422 TGGAGGACCACTTGAGACTGCCCTCTCCGTCATGAGCTAGAGCTAGGAAGACAACTAATGT 481	
Qy	528 TGAAGCTTGTGAGATCTTAAAGAAAGAGAGAAATGCTGAAAGAGAGAACCAAGTGT 587	
Db	482 TGAAGCTTGTGATAGCTTCAAGAAAGAGAGAAATGCTGAAAGAGAGAACCAAGGTT 541	
Qy	588 TGGTAGCCAGATGGAGATTAATCATCATGTGGAGCAGAGAGCTGAGATGAGATGTCAAC 647	
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Qy	648 CTGCTGACAAATCTCCGA---CAATCTCCGTCGACTCTCCACTACTTAATTAGCCAC 704	
Db	602 CACCTGACAAATCTTGACATCAATCGTCCGGTAACTCTCCGACTGCTTTATTAGCCAC 661	
Qy	705 CTTAAATCGCGGTTGAAATCAAAATCCAAA 736	
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XX	AAA29037 standard; cDNA; 990 BP.	
AC	AAA29037;	
XX	12-SEP-2000 (first entry)	
DT		
XX		
DE	B. napus flowering locus F (FLF) homologous cDNA 6.	
XX		
KW	Flowering locus F; transcription factor; DNA binding domain; MADS box;	
KW	FLF; chromosome 5; RFLP marker 447; flowering time; vernalization; ss.	
OS	Brassica napus.	
XX		
PH	Key Location/Qualifiers	

FT	CDS	30..664	
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XX		/product= "FLF_homologue"	
PN	WO200032780-A1.		
PD	08-JUN-2000.		
PP	02-DEC-1999; 99WO-AU001079.		
XX			
PR	03-DEC-1998; 98AU-00007469.		
PR	22-JAN-1999; 99US-0116928P.		
XX	(CSIR) COMMONWEALTH SCI & IND RES ORG.		
FA	(PERE) PEREZ P.		
XX			
PI	Perez P, Burn JB, Peacock WJ, Dennis ES, Sheldon CC;		
PI	Helliwell CA, Rouse DJ;		
XX			
DR	WPI; 2000-451762/39.		
XX	P-PSDB; AAY96413.		
PT	New nucleic acid comprising a MADS box that encodes a transcription		
PT	factor for altering the flowering time or modifying the vegetative or		
XX	floral phenotype of a plant such as wheat.		
XX	Claim 6; Page 88-89; 106pp; English.		
CC	AAA29032-41 are cDNA clones isolated from a Brassica napus cDNA library		
CC	using hybridisation to an FLF (flowering locus F) cDNA from Arabidopsis		
CC	thaliana. From both amino acid and nucleotide sequence data it was		
CC	concluded that the clones represent transcripts from 5 different genes.		
CC	The FLF gene encodes a transcription factor protein comprising a		
CC	distinctive conserved DNA binding domain (a MADS box). The DNA was		
CC	identified from a late-flowering mutant (flf) which arose during		
CC	transformation of the early-flowering ecotype C24 with a modified binary		
CC	vector pbin-delta-Ac. It was found that two T-DNAs segregate in the very		
CC	late flowering phenotype and that two expressed genes (A and B) were		
CC	closely linked to these T-DNAs. Gene B was re-designated as FLF. The FLF		
CC	gene is linked to the top of chromosome 5, 4 cm from RFLP marker 447. The		
CC	protein is capable of altering the flowering time of a plant. Over-		
CC	expression of the FLF gene can be used to delay flowering in a plant.		
CC	Alternatively, reduction of FLF gene expression, e.g. by antisense		
CC	constructs, can be used to induce early flowering. Methods of modifying		
CC	vegetative and/or floral phenotypes of a plant comprising increasing the		
CC	level of expression of a FLF gene to modify the production or activity of		
CC	a gibberellin in the plant are also claimed. The response of a plant to		
CC	vernalization can also be altered. Any dicotyledonous or monocotyledonous		
CC	plant species including horticultural plants, particularly those in the		
CC	cut-flower industry, vegetable, cereal and other crop plants are capable		
CC	of being controlled		
XX			
SQ	Sequence 990 BP; 289 A; 209 C; 223 G; 269 T; 0 U; 0 Other;		
Query Match			
Best Local Similarity 51.3%; Score 484; DB 3; Length 990;			
Matches 635; Conservative 0; Mismatches 145; Indels 14; Gaps 5;			
Qy	85 CACAAAGCCCTCTCGGAGAGAGCCCTGGAAGAAAAGAAAAGAAAAGAAAAGAAAAGTGA 144		
Db	6 CAGAGACCCTCTGGAGACAGAAACCTTCTGGAAGAAAAGAAAAGAAAAGAAAAGTGA 65		
Qy	145 GAACAAAAGTAGCGCAGCAAGTCACTTCTCAAAACGTGCGCAACGGTCTCTCGAAGAAAGC 204		
Db	66 GAACAAAAGTAGCGCAGCAAGTCACTTCTCAAAACGAGCAGCGGTCTCTATTGAAAGC 125		
Qy	205 TCGTCAGCTTTCTGTTCTCTGTGACGATCCGTGCTCTTCTCGTCTCTCTCCGCTCCGG 264		
Db	126 TCGTCAGCTTTCTGTTCTCTGTGATGATCGTCCGCTCTCTGTTCTCTCTCTCCG 185		
Qy	265 CAAGCTCTACAGCTTCTCTCTCCGCGATACCTGCTCAAGATCTTTCATGATATGGAA 324		
Db	186 CAAGCTCTACAGCTTCTCTCCGCGGTGATAACCTGGTGGATCTTTCATGATATGGAA 245		

Qy	325	ACAGCATGCTGATGATCTTAAAGCCTTGGATCATAGTCAAAAGCTCTGAACCTATGGTTC	384
Db	246	ACAGCATGCTGATGATCTTAAAGCCCTGATCTTCAGTCAAAAGCTCTGAGCTATGGTTC	305
Qy	385	ACACTATGAGCTACTTGAACCTTGGATAGCAAGCTTGTGGATCAAAATGTCAAAAATGT	444
Db	306	ACAAATGAGTTACTTGAACCTTGGATAGCAAGCTTGTGGATCAAAATGTCGGTGGTGT	365
Qy	445	GAGTATCGATGCTCTTGTTCAACTGGAGGAACACCTTGGAGCTGCCCTCTCCGTGACTAG	504
Db	366	AAGCGTGGACACCCCTCGTTGAGCTGGAGGGTGTCTTGAATAATGCCCTCTCTTAAGTAC	425
Qy	505	AGCAAGAAGACCGAACTCATGTGTGAAGCTTGTGTGAATCTTAAAGAAAAGGAGAAAT	564
Db	426	AGCTAGGAAGACAGAACTATGTGTGAAGCTTGTGTAGCTCTAAAGAAAAGGAGAGCT	485
Qy	565	GCTGAAGAAGAGAAACAGGTTTGGCTAGCCAGATGGAGAAATAATCATCATGTGGGAGC	624
Db	486	GCTGAAGAAGAGAAATCAGGCTTGGCTGGCCAGAGGAGAGAGAAATCTTGGGGAGC	545
Qy	625	AGAAGCTGAGATGGAGATGTCACCTGCTGGACAAATCTCCGA---CAATCTTCGGGTGAC	681
Db	546	CGAAGCTGATAATATGGAGATGTCACCTGGACAAATCTCCGACATCAATCTTCGGGTAC	605
Qy	682	TCTCCCACTACTTAATTAGCCACCTTAAATCGCGGTTGAAATCAAAATCAAAACATAT	741
Db	606	TCTCCCACTGCTTAATTAGCCACCGTTAGACGGGGCT--GATCAAAATTAATAAATCCAA	662
Qy	742	ATAATTATGAAGAAAAAATAAGATATGTAAATTATTCGCTGTATAGGGCGAGCGTT	801
Db	663	AACAT----ACAATAAATAAAGCTTTTGTGTTTTCACCCCTTGAAGGGTGACAG-T	717
Qy	802	TGTATATCTTAATACTCTCTTTGGCCAGAGACTTTGTGTGTATACTTTAAGTAGACG	861
Db	718	TGTATATCTCAATACTC---CCTTGGCTGAGAGATTGTGTGTACTCTCTATGTATAGATA	774
Qy	862	GAACTAAGTCAATA	875
Db	775	TAATGAGTAAATA	788

Search completed: May 22, 2006, 05:31:47
Job time : 649 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 05:32:03 ; Search time 4482 Seconds
(without alignments)
11765.268 Million cell updates/sec

Title: US-09-857-346A-2
Perfect score: 943
Sequence: 1 cgagaaaggagaaaaaa.....tgagaaaaaa 943

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: gb_est1:*
 - 2: gb_est3:*
 - 3: gb_est4:*
 - 4: gb_est5:*
 - 5: gb_est6:*
 - 6: gb_hic:*
 - 7: gb_est2:*
 - 8: gb_est7:*
 - 9: gb_est8:*
 - 10: gb_est9:*
 - 11: gb_gss1:*
 - 12: gb_gss2:*
 - 13: gb_gss3:*
 - 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	593.4	62.9	941	10	DR749990 81-L02009
2	590.8	62.7	899	10	DR749991 81-L02009
3	578.2	61.3	595	10	DR376425 110426 CE
4	507.4	53.8	769	8	CX267207 38RDBRM U
5	499.2	52.9	503	9	DR198395 1106125 C
6	487.4	51.7	701	8	CN730669 24RDBNH U
7	458.8	48.7	609	5	CD816564 EN20.001A
8	417.8	44.3	606	8	CN737667 26RDBNT U
9	406.8	43.1	419	9	DR198394 73477 CER
10	372.4	39.5	655	9	DR262234 12822141
11	370.8	39.3	640	1	AU238414 10238414
12	362.8	38.5	673	4	CA781283 014D08AF
13	345.2	36.6	936	10	DR751518 02-L02009
14	344.2	36.5	896	10	DR751519 02-L02009
15	338.4	35.9	679	8	CN828657 EL3007R B
16	336.4	35.7	554	1	AU235862 AU235862
17	334	35.4	594	11	B27231 T32A5TF TAM
18	315.2	33.4	401	2	BG544805 E2809 Chi
19	302.2	32.0	396	2	BG544804 E2808 Chi

20	301	31.9	465	9	DN925811	RS8nr005	
21	299	31.7	492	10	DR350810	971479 CE	
22	298.2	31.6	688	5	CD834584	BN45.042F	
23	295	31.3	727	8	CN736440	26RDBNT U	
24	294.2	31.2	699	4	CB257827	44-E01373	
25	290.8	30.8	919	10	DR749853	89-L02009	
26	290.8	30.8	921	10	DR750371	58-L02009	
27	281.2	29.8	492	9	DR262235	139397 CE	
C	28	276.6	29.3	882	10	DR750372	58-L02009
29	269.8	28.6	474	9	DR262237	112398 CE	
30	267.2	28.3	720	7	BE038655	AB03F04 A	
31	263.2	27.9	520	9	DR210837	131023 CE	
C	32	247.8	26.3	659	10	DR749854	89-L02009
33	246.2	26.1	690	3	BP796166	BP796166	
34	222.4	23.6	398	5	CD825381	BN25.050J	
35	218	23.1	469	1	AV553913	AV553913	
36	218	23.1	609	1	AU238299	AU238299	
37	218	23.1	662	10	DR369010	12831082	
38	209.4	22.2	353	8	CX269606	38RDBRM U	
C	39	209	642	11	BZ468975	BOOAL577R	
40	207	22.0	352	9	DR262232	45231424 C	
C	41	204.8	21.7	431	11	B96749	T32A4TF TAM
42	190	20.1	756	11	BZ069163	1KH07F11..	
43	188.6	20.0	420	10	DR369009	6637184 C	
44	184.6	19.6	434	1	AI994942	701500471	
45	184.2	19.5	585	10	DR378623	972305 CE	

ALIGNMENTS

RESULT 1
DR749990

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

DR749990 81-L020098-065-001-All-Sela MP1Z-ADIS-065d Arabidopsis thaliana
cDNA clone 001-All, mRNA sequence.

DR749990 941 bp mRNA linear EST 19-JUL-2005
DR749990.1 GI:71035330

Arabidopsis thaliana (chale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 941)
Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B.,
Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R.,
Coupland, G., Martin, C., Angenot, G.C., Baumlein, H., Mock, H.P.,
Carbonero, P., Colombo, L., Tonelli, C., Engstrom, P.,
Droge-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M.,
Laux, T., Hordasewski, M., Ruberti, I., Ratcliff, P., Smeekens, S.,
Somesich, I., Weishaar, B. and Traas, J.

REGIA, an EU project on functional genomics of transcription
factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002)

Contact:
Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski, Coupland, Martin, Angenot, Baumlein, Carbonero, Colombo, Tonelli, Engstrom, Droge-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Hordasewski, Ruberti, Smeekens, Somssich, Weishaar, Traas
RUBERTI, Smeekens, Somssich, Weishaar, Traas
Bielefeld University, Institute for Genome Research
Universitaetstrasse 25, D-33594 Bielefeld, Germany
Email: bernd.weishaar@uni-bielefeld.de

AGI: AT5G10140; SeqAnalysis: full CDS correct; Translation: full
good
Data analysis performed in the frame of REGULATORS (Exploiting inter-species conservation in promoter sequences to identify regulators of reproductive development and physiological performance), a Trilateral Co-Operation in Plant Genomics between Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent Thareau (IBP-Orsay UMR8618 CNRS-UPS, Thareau-ad-ibp.u-psud.fr) and Alain Lecharny (URGV-EVRY UMR INRA-CNRS-UEVE,

lecharny-ad-ibp.u-paud.fr).
 Definition of the terms used to describe the quality of the clone:
 The about 2250 sequences from the clone collection were sorted
 according to clones and clustered. If more than one contig was
 formed, the clone was designated 'Contamination'. The contigs and
 singletons were blasted against CDS plus pseudogenes from the
 TIGRv5 annotation, and the resulting AGI code is presented if more
 than 90 percent identity was found. The sequences were also blasted
 against all TIGRv5 introns, and matches longer than 50 bp with 95
 percent identity are reported as 'intron found'. The remaining
 terms for SeqAnalysis describe the outcome of the evaluation of the
 CDS detected after pairwise alignment with CDS plus pseudogenes
 from the TIGRv5 annotation file. The sequences or contigs for which
 a full CDS with or without STOP codon was detected, a BLASTp
 against all TIGRv5 protein sequences was performed. Full perfect:
 100 percent identity; full good: better than 95 percent identity
 over more than 95 percent of the sequence; partial good: better
 than 95 percent identity over less than 95 percent of the sequence;
 weak similarity: less than 95 percent identity over less than 95
 percent of the sequence; no similarity: no hit from BLASTp. Note
 that the collection contains a few clones for which sequencing was
 not successful, which could have simple technical reasons.
 Obviously, information about these clones is missing in the
 submitted data.

Insert Length: 941 Std Error: 0.00

Seq primer: Seta TCGCGTTACGCTAGCATGATCTC.

FEATURES source

Location/Qualifiers
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 /mol_type="mRNA"
 /ecotype="Columbia"
 /db_xref="GABI:1452167"
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 /clones="001-All"
 /lab_host="E. coli DH5alpha"
 /clone_lib="MP1Z-ADIS-065d"
 /note="Vector: pDONR201; In the context of the EU-funded
 project REGIA (OLG-CT11999-00876, coordinator Javier
 Paz-Ares), a set of transcription factor ORFs was
 generated. The ORFs were produced in a decentralized way
 in the labs of the participants. Most of the ORFs were
 generated by RT-PCR using cDNA from various A. thaliana
 tissues as a template. Initially, it was planned to use
 yeast recombination to move the ORFs from the cloning
 vectors into target constructs. For this reason, a number
 of the clones contain 'REGIA tags' (RG_tag):
 Spr-AATTCAGTCCACCACC-3pr; RG_tag:
 Spr-CATGGCAATCCGGGATC-3pr). During the lifetime of the
 project, the GATEWAY system became available and finally
 all ORFs were transferred into GATEWAY vectors. At the end
 of the REGIA project, the clones were collected as plasmid
 DNA. For end-sequencing at the DNA core facility of the
 MPI of Plant Breeding Research (ADIS; head: Bernd
 Weisshaar), the plasmids were re-transformed into
 DH5alpha, arrayed into 96-well plates and new plasmid DNA
 was prepared. Re-transformation proved to be difficult
 because a number of clones displayed poor growth. Data
 submission has been handled by GabiPD
 (<http://gabi.rzpd.de/>)."

ORIGIN

Query Match 62.9%; Score 593.4; DB 10; Length 941;
 Best Local Similarity 99.0%; Pred. No. 5.6e-142;
 Matches 597; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 98 CGGAGAGAGCCATGGGAGAGAAAAAATTAGAAATCAAGCGAATTCAGAACAAAAGTAGC 157
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 DB 83 CGGGTATTCACCATGGGAGAGAAAAAATTAGAAATCAAGCGAATTCAGAACAAAAGTAGC 142
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 QY 158 CGACAGTACCTTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTGCTGAGCTTTCT 217
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 DB 143 CGAAGTACCTTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTGCTGAGCTTTCT 202
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QY 218 GTTCTCTGTGACGATCCGCTGCTCTTCTCGTCTCCGCTCCGCGCAAGCTCTACAGC 277
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 DB 203 GTTCTCTGTGACGATCCGCTGCTCTTCTCGTCTCCGCTCCGCGCAAGCTCTACAGC 262
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 QY 278 TTCTCTCCGCGGATAACTGGTCAAGATCTCTTGATCGATATGGGAAACAGCATGCTGAT 337
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 DB 263 TTCTCTCCGCGGATAACTGGTCAAGATCTCTTGATCGATATGGGAAACAGCATGCTGAT 322
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 QY 338 GATCTTAAGCCCTGGATCATCATGATCAAAAGCTCTGAATATGGTTCACTATGAGCTA 397
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 DB 323 GATCTTAAGCCCTGGATCATCATGATCAAAAGCTCTGAATATGGTTCACTATGAGCTA 382
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 QY 398 CTTGAACCTTGTGATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCT 457
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 DB 383 CTTGAACCTTGTGATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCT 442
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 QY 458 CTTGTTTCACTGGAGGAACACCTTGAGATCGCCCTCTCCGTGACTAGAGCCAAAGAGACC 517
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 QY 518 GAACATGTTGAGCTTGTGAGATCTTAAAGAAAGAGAAAATGCTGAAAGAGAG 577
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 DB 683 TAG 685

RESULT 2
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 cDNA clone 001-All, mRNA sequence.
 DR749991
 ACCESSION
 DR749991.1 GI:71035331
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 899)
 Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B.,
 Gilmarin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R.,
 Coupland, G., Martin, C., Angenent, G. C., Baumelein, H., Mock, H. P.,
 Carbonero, P., Colombo, L., Tonelli, C., Engstroem, P.,
 Droge-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M.,
 Laux, T., Hordworth, M., Ruberti, I., Ratcliff, P., Smeekens, S.,
 Somsch, I., Weisshaar, B. and Traas, J.
 REGIA, an EU project on functional genomics of transcription
 factors from Arabidopsis thaliana
 Comp. Funct. Genomics 3 (2), 102-108 (2002)
 Contact:
 Paz-Ares, Costantino, Vittorioso, Davies, Gilmarin, Giraudat, Parcy, Sabl
 owski, Coupland, Martin, Angenent, Baumelein, Carbonero, Colombo, Tonelli,
 Engstroem, Droge-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Hordsworth
 Ruberti, Smeekens, Somsch, Weisshaar, Traas
 Bielefeld University, Institute for Genome Research
 Universitaetsstrasse 25, D-33594 Bielefeld, Germany
 Email: bernd.weisshaar@uni-bielefeld.de
 AGI: AT5G10140; SeqAnalysis: full CDS correct; Translation: full
 good
 Data analysis performed in the frame of REGULATORS (Exploiting
 inter-species conservation in promoter sequences to identify

regulators of reproductive development and physiological performance), a Trilateral Co-Operation in Plant Genomics between Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent Thureau (IBP-Orsay UMR8618 CNRS-UPS, thureau-ad-ibp.u-psud.fr) and Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE, lecharny-ad-ibp.u-psud.fr).

Definition of the terms used to describe the quality of the clone: The about 2250 sequences from the clone collection were sorted according to clones and clustered. If more than one contig was formed, the clone was designated 'Contamination'. The contigs and singletons were blasted against CDS plus pseudogenes from the TIGRv5 annotation, and the resulting AGI code is presented if more than 90 percent identity was found. The sequences were also blasted against all TIGRv5 introns, and matches longer than 50 bp with 95 percent identity are reported as 'intron found'. The remaining terms for SeqAnalysis describe the outcome of the evaluation of the CDS detected after pairwise alignment with CDS plus pseudogenes from the TIGRv5 annotation file. The sequences or contigs for which a full CDS with or without STOP codon was detected, a BLASTp against all TIGRv5 protein sequences was performed. Full perfect: 100 percent identity; full good: better than 95 percent identity over more than 95 percent of the sequence; partial good: better than 95 percent identity over less than 95 percent of the sequence; weak similarity: less than 95 percent identity over less than 95 percent of the sequence; no similarity: no hit from BLASTp. Note that the collection contains a few clones for which sequencing was not successful, which could have simple technical reasons. Obviously, information about these clones is missing in the submitted data.

Insert Length: 899 Std Error: 0.00
Seq primer: SELB GTACATCAGAGATTGAGACAC.
Location/Qualifiers
1.899

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/mol_type="mRNA"
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/db_xref="taxon:3702"
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/clone_lib="MP12-ADIS-065d"
/note="Vector: pDONR201. In the context of the EU-funded project REGIA (QIG-CT1199-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag1: 5pr-AATCCAGCTCACACC-3pr; RG_tag2: 5pr-CATGCAATTCGGGGATC-3pr). During the lifetime of the project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS; head: Bernd Weisshaar), the plasmids were re-transformed into DH5alpha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GabiPD (http://gabi.rzpd.de)."

ORIGIN
Query Match 62.7%; Score 590.8; DB 10; Length 899;
Best Local Similarity 96.5%; Pred. No. 2.6e-141;
Matches 604; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
98 CGGAGAGAGCCATGCGAGAGAAAACTGAAATCAGCGAATGAGCAAAAGTAGC 157
|||||

Db 721 CGGGAATTCACCTCGGAGAAAAAACTAGAAATCAAGCGAATGAGAACAAAAAGTAGC 562
Qy 158 CGAAGATCAGCTTCTCCAAACGTCGCAACCGTCTCATCGAGAAAGCTGTCAGCTTTCT 217
Db 661 CGAAGATCAGCTTCTCCAAACGTCGCAACCGTCTCATCGAGAAAGCTCGTCAGCTTTCT 602
Qy 218 GTTCTGTGAGCAGCATCGCTCTTCTCTCGTCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 277
Db 601 GTTCTGTGAGCAGCATCGCTCTTCTCTCGTCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 542
Qy 278 TTCTCTCCCGCGGATTAACCTCGTCAAGATCCTTGAATCGATATGGGAAAACAGATGCTGAT 337
Db 541 TTCTCTCCCGCGGATTAACCTCGTCAAGATCCTTGAATCGATATGGGAAAACAGATGCTGAT 482
Qy 338 GATCTTAAAGCCTTGGATCATCATGATCAAAAGCTCTGAAGTCTGAACTATGTTCACTATGAGCTA 397
Db 481 GATCTTAAAGCCTTGGATCATCATGATCAAAAGCTCTGAAGTCTGAACTATGTTCACTATGAGCTA 422
Qy 398 CTTCGAATCTGGATAGCAAGCTTGTGGATCAAAATGTCAAAATGTCAAAATGTCAAAATGTCAAAATGT 457
Db 421 CTTCGAATCTGGATAGCAAGCTTGTGGATCAAAATGTCAAAATGTCAAAATGTCAAAATGTCAAAATGT 362
Qy 458 CTTCGTTCAACTGGAGGAACACCTTTGAGACTGCTCCCTCTCCGTCGCTAGAGCCAAAGAGACC 517
Db 361 CTTCGTTCAACTGGAGGAACACCTTTGAGACTGCTCCCTCTCCGTCGCTAGAGCCAAAGAGACC 302
Qy 518 GAATCATGTTGAAAGCTTTGTTGAGAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAG 577
Db 301 GAATCATGTTGAAAGCTTTGTTGAGAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAG 242
Qy 578 AACCAGCTTTGGCTAGCCAGATGAGAAATATCATGTTGGGAGCAAGAGCTGAGATG 637
Db 241 AACCAGCTTTGGCTAGCCAGATGAGAAATATCATGTTGGGAGCAAGAGCTGAGATG 182
Qy 638 GAGATGTCACCTGCTCGACAAATCTCGACAAATCTTCGGTGACTCTCCGTCGCTACTCTCCACTTCTTAAT 697
Db 181 GAGATGTCACCTGCTCGACAAATCTTCGGTGACTCTTCGCAAAATCTTCGGTGACTCTCCGTCGCTACTTAAAT 122
Qy 698 TAGCCACCTTAAATCGGGGTTGAAA 723
Db 121 TAGGTCGAGGGAATCACTAGTTATAA 96

RESULT 3
DR376425
LOCUS
DEFINITION 110426 CERES-148 Arabidopsis thaliana cDNA clone 39347 3', mRNA
ACCESSION DR376425
VERSION DR376425.1
KEYWORDS EST, GI:86080668
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 595)
AUTHORS Alexandrov,N.N., Troukhan,M.E., Brover,V.V., Tatarinova,T., Lu,Y.-P., Flavell,R.B. and Feldmann,K.A.
TITLE Features of Arabidopsis genes and genome discovered using full-length cDNAs
JOURNAL Plant Mol. Biol. 60 (1), 71-87 (2006)
COMMENT Contact: Alexandrov NN
Ceres, Inc
1535 Rancho Conejo Blvd., Thousand Oaks, CA 91320, USA
Tel: (805) 376-6539
Fax: (805) 498-1002
Email: naalexandrov@ceres-inc.com.
Location/Qualifiers
1.595
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Mixed, WS and Landsberg erecta"

/db_xref="taxon:3702"
/clone="39347"
/tissue type="Mixed floral buds, roots (9:1)"
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ORIGIN
Query Match 61.3%; Score 578.2; DB 10; Length 595;
Best Local Similarity 99.2%; Pred. No. 4.3e-138;
Matches 592; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 158 CGCAAGTCACCTTCCAAACGTCGCAACGGTCTCATCGAAGAGCTCGTCAGCTTTCT 217
Db 1 CGCAAGTCACCTTCCAAACGTCGCAACGGTCTCATCGAAGAGCTCGTCAGCTTTCT 60
QY 218 GTTCTCTGTGACGATCCGTCGCTCTTCTGTGCTCTCCGCTCCGCGCAAGCTCTACGC 277
Db 61 GTTCTCTGTGACGATCCGTCGCTCTTCTGTGCTCTC--CCTCGGCAAGCTCTACGC 118
QY 278 TTCTCTCCGCGGATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGAT 337
Db 119 TTCTCTCCGCGGATAACCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGAT 178
QY 338 GATCTTAAGCCTTGGATCATCAGTCAAAAGCTCTGAATATGGTTTCACTATGAGCTA 397
Db 179 GATCTTAAGCCTTGGATCATCAGTCAAAAGCTCTGAATATGGTTTCACTATGAGCTA 238
QY 398 CTTGAACTTGTGGATAGCAAGCTTGTGGATCAAAATGTCAAAATGTGAGTATCGATGCT 457
Db 239 CTTGAACTTGTGGATAGCAAGCTTGTGGATCAAAATGTCAAAATGTGAGTATCGATGCT 298
QY 458 CTTGTTTCAACTGGAGGAACCTTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAGACC 517
Db 299 CTTGTTTCAACTGGAGGAACCTTTGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAGACC 358
QY 518 GAATCATGTTGAAGCTTGTGAGAACTTAAAGAAAGAGAGAAATGCTGAAAGAGAG 577
Db 359 GAATCATGTTGAAGCTTGTGAGAACTTAAAGAAAGAGAGAAATGCTGAAAGAGAG 418
QY 578 AACAGGTTTGTGCTAGCAGATGGAGAAATATCATCATGTGGGAGCAGAGCTGAGATG 637
Db 419 AACAGGTTTGTGCTAGCAGATGGAGAAATATCATCATGTGGGAGCAGAGCTGAGATG 478
QY 638 GAGATGTACCTCTGGACAAATCTCCGACAACTTTCCGCTGACTCTCCCACTACTTAAT 697
Db 479 GAGATGTACCTCTGGACAAATCTCCGACAACTTTCCGCTGACTCTCCCACTACTTAAT 538
QY 698 TAGCCACCTTAATCCGCGGTTGAAATCAAATCAAACATATATATTAAGA 754
Db 539 TAGCCACCTTAATCCGCGGTTGAAATCAAATCAAACATATATATTAACAAAA 595

RESULT 4
CX267207
LOCUS
DEFINITION
38RDBRM UP_019 C08 02APR2004_060 Brassica rapa 38RDBRM Brassica
rapa cDNA 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa (Brassica campestris)
Brassica rapa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1. (bases 1 to 769)
Xiang,D., Venglat,P., Keller,G., Selvaraj,G. and Datla,R.
Gene Expression Patterns during Brassica Zygotic Embryogenesis
Unpublished (2004)
Contact: Raju Datla
Molecular and Developmental Genetics
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada

Tel: 306 975 5267
Fax: 306 975 4839
Email: Raju.Datla@nrc-cnrc.gc.ca
High quality sequence stop: 769.

FEATURES
Source

1. .769
Location/Qualifiers
/organism="Brassica rapa"
/mol_type="mRNA"
/db_xref="taxon:3711"
/clone_lib="Brassica rapa 38RDBRM"
/notes="Vector: pDNR-LIB CREATOR; Site 1: Sfi 1A; Site 2:
Sfi 1B; Brassica rapa 38RDBRM. Sequences have been trimmed
to remove vector and low quality regions using LUCY
sequence cleanup software (www.tigr.org)."

ORIGIN

Query Match 53.8%; Score 507.4; DB 8; Length 769;
Best Local Similarity 83.5%; Pred. No. 9.1e-120;
Matches 624; Conservative 0; Mismatches 116; Indels 7; Gaps 4;
QY 5 AAAGGAAAAAATAAGAAAGAGAAAAAGC--TTAGTATCTCCGGCGACTTGAACCCA 63
Db 23 AAAGGAAAAAATAAGAAAGAGAAAAAGCATAAAACGCTTTAGTATCTCCGGCGACTTGA 81
QY 64 AACCTCAGGATCAAAATAGGGCAAAAGCCCTCTCGAG--AGAAGCCATGGGAAGAAA 121
Db 82 AACCTCTGGATCAAAATAGGGCAAGAGACCACTTGGAGACAAACCATGGGAAGAAA 141
QY 122 AAACCTAGAAATCAAGCGAATTTAGAGAACAAAGTAGCCCAAGTCACTCTTCTCCAAACGT 181
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QY 182 CGCAACGGTCTCATCGAGAAAGCTCGTCACTTTCTGTCTCTGTGACGATCCGTCGCT 241
Db 202 CGCAGCGGCTCATTTGAGAAAGCTCGTCACTTTCTGTCTCTGTGACGATCCGTCGCG 261
QY 242 CTTCTCGTCTCGCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGCGGAGTAACCTGGTC 301
Db 262 CTTCTCGTCTCTCTCTCTCCGCAAGCTCTACAGCTTCTCTCCGCGGAGTAACCTGGTC 321
QY 302 AAGATCTTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCCTTGGATCATCAG 361
Db 322 AAGATCTTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCCTTGGATCATCAG 381
QY 362 TCAAAAGCTCTGAACATATGTTTCACTATGAGCTACTTGAACCTTGTGATAGCAAGCTT 421
Db 382 TCANAAGCTCTGAGCTATGGTTTCACTATGAGTTACTTTGAACTTGTGATAGCAAGCTT 441
QY 422 GTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTTGTTCAACTGGGGAACACCTT 481
Db 442 GTGGGATCAAAATGTGAGTATCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGCTT 501
QY 482 GAGACTGCCCTCTCCGTGACTAGAGCAAGAGACCGAACTCATGTTGAAGCTTGTGAG 541
Db 502 GAAATGCCCTCTCTCTAACTAGAGCTAGGAGACAGAACTAATGTTGAAGCTTGTGAT 561
QY 542 AATCTTAAAGAAAGAGAGAAATGCTGAAAGAGAGAACAGGTTTGTGCTAGCCAGATG 601
Db 562 AGCCTCAAGAAAGAGAGAGAGCTGCTGAAAGAGAGAAATCAGGCTTTGGCTGGCCAGAAG 621
QY 602 GAGAAATATCATCATGTGGGAGCAGAGCTGAGATGATGATGAGATGATGATGAGATGATG 661
Db 622 GAGAAAGAAATCTTTGGGAGCCGAGCTGATATATATGAGATGATGATGATGATGATGATG 681
QY 662 TCCGA---CAATCTTCCGGTGAATCTCCCACTACTTAAATAGCCACCTTAAATCGCGGT 718
Db 682 TCCGACATCAATCTTCCGGTAACTCTCCCACTACTTAAATAGCCACCTTAAATAGCGGGCT 741
QY 719 TGAATCAAAATCCAAACATATATAA 745
Db 742 GATCAATTTAAAAAATCCAAACATACAA 768

Db	364	AGGAATCAAAATGTCGTAATGTAAGTGTGGGTTCCCTGGTTTCAGCTGGAGAAACACCTTG	423
QY	483	AGACTGCCCTCTCCGTGACTAGAGCCCAAGAGACCGAACTCAGTGTGAAGCTTGTGAGA	542
Db	424	AGAACGCCCTCTCCGTAACAAAGAGCTAGGAAGACAGAACTAATGTTGAAGCTTGTGAGA	483
QY	543	ATCTTAAAGAAAAGAGAAATGCTGAAAGAGAGAACCAAGGTTTTTGGCTAGCCAGATGG	602
Db	484	ACCTTAAAGAAAAGGAGAGTGTCTGGNAGAGAGAGAACCATGTTTTTGGCTAGCCAGATGG	543
QY	603	AGAAATATCATATGTGGAGAGCAAGAGCTGAGATGGAGATGTCACTGTGGACAAA---	659
Db	544	AGAAGAGTAAATCTTGTGCGAGCGGAGCTGATATATATGAGGTTGTCACTGGACAAAATC	603
QY	660	-TCTCGACAACTTCCGGTGACTCTCCCACTACTTAATATAGCCACTTAATATCGGGGT	718
Db	604	TCCGACATCAATCTTCTGGTAACGCTCCCACTGCTTAATATAGTTACCGTTAATTCGGCGAA	663
QY	719	TGAATCAAAATCCAAAACATATATATATGAAGAA	755
Db	664	TAAATAAATCCAAACATATTAATTAACAACAA	700
RESULT 7			
LOCUS	CD816564	609 bp mRNA linear	EST 10-JUL-2003
DEFINITION	BN20_001A12F010914 BN20 Brassica napus cDNA clone BN20001A12, mRNA sequence.		
ACCESSION	CD816564		
VERSION	CD816564.1	GI:32498504	
KEYWORDS	EST.		
SOURCE	Brassica napus (rape)		
ORGANISM	Brassica napus		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.		
AUTHORS	1 (bases 1 to 609)		
TITLE	Genoplante.		
JOURNAL	Genoplante, a major partnership french program in plant genomics		
COMMENT	Unpublished (2003)		
CONTACT	Contact: Genoplante		
Genoplante	93, rue Henri Rochefort 91025 EVRY CEDEX France		
Tel:	33 1 69 47 54 00		
Fax:	33 1 69 47 54 10		
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com) and http://genoplante-info.infobiogen.fr .			
FEATURES	Location/Qualifiers		
source	1..609		
/organism="Brassica napus"			
/mol_type="mRNA"			
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Best Local Similarity	86.7%;	Pred. No. 3.1e-107;	
Matches 517; Conservative	0;	Mismatches 77;	Indels 2; Gaps 1;
QY	75	CAAAATTAGGGCAAAAGCCCTCTCGAG--AGAAGCCATGGGAAGAAAAAACTAGAAT	132
Db	1	CAAAATTAGGGCGCAAGCCCGTTGGAGACAGAAGCATGGGAGAAAGAACTTGAAT	60
QY	133	CAAGCGAATTGAGAACAAAGTAGCCGACACTCTCCAAAGCTGCAACGGTCT	192
Db	61	CAAGCGATTGAGAACAAAGTAGCCGACAGTTACCTTCTCCAAACGACGCAACGGTCT	120
QY	193	CATCGAGAAAGCTCGTCAGCTTTCTGTTCTGTGACGCATCCGTCGCTCTTCTCGTCT	252
Db	121	CATCGAGAAATGCTCGTCAGCTTTCCGTTCTCTGTGACGCATCGTCGCTCTTCTGTGCT	180
QY	253	CTCCGCTCCGCGACAGCTCTACAGCTTCTCCTCCGCGGATAACCTGGTCAAGATCCCTGA	312
Db	181	CTCCGCTCCGCGAACTCTACAGCTTCTCCTCCGCGTATACCTGGTCAAGATCCCTGA	240
QY	313	TGATATATGGAACACAGCATGCTGATGATCTTAAAGCTTTGGATCATCAGTCAAAAGCTCT	372
Db	241	TGATACGGAAGCAACATGGTATGATCTTAAAGCTTTGGATCGTCAGTCAAAAGCTTT	300
QY	373	GAACTATGTTTCACTATGACTACTTGAACCTTGTGGATAGCAAGCTTGTGGATCAAA	432
Db	301	GGACTCTGTTTCACTACCATGAGCTGTGAACTTGTGGAAAGCAAGCTTGAGGAATCAAA	360
QY	433	TGTCAAAATGTGAGTATCGATGCTTGTTCATCTGGAGGACACCTTGAGATCGCCT	492
Db	361	TGTGATATATGAGTGTGGTTTCCCTGCTCAGCTGGAGGAACACCTTTGAGAACGCCCT	420
QY	493	CTCCGTGACTAGAGCCAAAGAACCGAACTCATGTTTGAAGCTTGTGAGAACTTAAAGA	552
Db	421	CTCCGTAAACAGAGCTAGGAACAGAACTAATGTTGAAGCTTGTGAGAACCTTAAAGA	480
QY	553	AAAGGAGAAATGCTGAAAGAGAGAACCAAGTTTTTGGCTAGCCAGATGGAGAAATATCA	612
Db	481	AAAGGAGAAATGCTGGAAGAGGAGAACCATGTTTGGCTAGCCAGATGGAGAGATTA	540
QY	613	TCATGTGGAGCAGAGCTGAGATGGAGATGTCACCTGCTGGACAAATCTCCGACA	668
Db	541	TCTTGTGAGCCGAGCTGATATATGAGGTTGTCACCTGGACAAATCTCCGACA	596
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LOCUS	CN737667	606 bp mRNA linear	EST 14-MAY-2005
DEFINITION	26RDBNT UP 029_E02_23JAN2004_008 Brassica napus 26RDBNT Brassica napus cDNA 5', mRNA sequence.		
ACCESSION	CN737667		
VERSION	CN737667.1	GI:65295486	
KEYWORDS	EST.		
SOURCE	Brassica napus (rape)		
ORGANISM	Brassica napus		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.		
AUTHORS	Xiang,D., Venglat,P., Keller,G., Selvaraj,G. and Datla,R.		
TITLE	Gene Expression Patterns during Brassica Zygotic Embryogenesis		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: Raju Datla		
Molecular and Developmental Genetics			
National Research Council of Canada			
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,			
Saskatchewan, S7N 0W9, Canada			
Tel:	306 975 5267		
Fax:	306 975 4839		
Email:	Raju.Datla@nrc-cnrc.gc.ca		
High quality sequence stop: 606.			
Location/Qualifiers			
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/db_xref="taxon:3708"			
/clone_lib="Brassica napus 26RDBNT"			
/note="Vector: pDNR-LIB CREATOR; Site_1: Sfi IA; Site_2: Sfi IB; Zygotic embryos at torpedo stage from Brassica napus seeds were used for the isolation of PolyA RNA and in the construction of the cDNA library. Sequences have been trimmed to remove vector and low quality regions using LUCY sequence cleanup software (www.tigr.org)."			
ORIGIN			
Query Match	44.3%;	Score 417.8;	DB 8; Length 606;


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Query Match      39.5%; Score 372.4; DB 9; Length 655;
Best Local Similarity 75.9%; Pred. No. 6.8e-85;
Matches 460; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

QY 104 GAAGCCATGGGAAGAAAAAATAGAAATCAAGCGAATTCAGAACAAAAGTAGCCGACAA 163
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QY 224 TGTGAGCCATCCGTCGCTCTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 283
DB 121 TGTGAATCTCCGTCGCTCGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 180
QY 284 TCCGGCGATAAACCCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTT 343
DB 181 TCCGGTGACGACATTTCCAGAAAGAAATTCGAGATCAAGCGAATTCGAGAACAAAAGTAGCCGACAA 60
QY 344 AAAGCCTTGGATCATCAGTCAAAAGCTCTGAACTATGTTTCACTATGAGCTTACTTGAA 403
DB 241 AGAGCCTTAGATCTTGAGAAAAAATTCAGAAATTAATCTCCACACAAAGGATTTACTAGAA 300
QY 404 CTTTGGATAGCAAGCTTTGTTGGGATCAATGTCAAAATATGTGAGTATCGATGCTTTGTT 463
DB 301 ACAGTCCAAAGCAAGCTTTGAAGAACAAATGTCGATATGTAAGTGTAGATCTCTTAAT 360
QY 464 CAACTGGAGGAACACCTTGAGACTCCCTCTCCGTCGTCGTCGTCGTCGTCGTCGTCGTC 523
DB 361 TCTCTGGAGGACAACTTGGAGACTGCTCTGTCGTAAGTAGACTAGGAGGCGAAGCTG 420
QY 524 ATGTTGAAGCTTTGAGAAATCTTAAAGAAAGGAGAAATCTGAAAGAAAGGAGAACACCA 583
DB 421 ATGATGGAGTATATCGAGTCCCTTAAAGAAAGGAGAAATTCCTGAGAGAGAGAACCA 480
QY 584 GTTTTGGCTAGCCAGATGGAGAAATTAATCATATGTGGGAGCAGAAAGCTGAGATGGAGATG 643
DB 481 GTTCTGGCTAGCCAGATGGAGAAAGAAATAGTGTGTCGGCAACAGATGATGAGAGAGAA 540
QY 644 TCACCTGCTGGNCAATCTCCGACAACTCTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 703
DB 541 TTTCCGGGAAGTAGCTCCGGCAACAAATACCGGAGACTCTCCGCTGCTCAATTAGCCA 600
QY 704 CCTTAA 709
DB 601 CCATCA 606

RESULT 11
AU238414 640 bp mRNA linear EST 01-APR-2002
LOCUS AU238414 RAFL17 Arabidopsis thaliana cDNA clone RAFL17-22-J12 5',
DEFINITION mRNA sequence.
ACCESSION AU238414
VERSION AU238414.1 GI:19877583
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 640)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J.,
Itoh, M., Iehi, Y., Arakawa, T., Shibata, K., Shinagawa, A.,
Muranatsu, M., Hayashizaki, Y., and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)
Contact: Motoaki Seki

FEATURES
source
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/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
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/lab_host="DH10B"
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/note="Site 1: BamHI; Site 2: SalI; Subtraction library.
The sequence was obtained from samples subjected to
dehydration-treated (1, 2, 5, 10 and 24 hr) and
dehydration-treated (1, 2, 5, 10, and 24 hr after
dehydration treatment)"

ORIGIN
Query Match      39.3%; Score 370.8; DB 1; Length 640;
Best Local Similarity 75.7%; Pred. No. 1.7e-84;
Matches 459; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 104 GAAGCCATGGGAAGAAAAAATAGAAATCAAGCGAATTCAGAACAAAAGTAGCCGACAA 163
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QY 164 GTCACTTTCTCCAAAGCGTCCAAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTC 223
DB 61 GTCACTTTCTCCAAAGCGCAATGGTCTCATCGACAAAGCTCGACAACTTTTCGATTCTC 120
QY 224 TGTGAGCCATCCGTCGCTCTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 283
DB 121 TGTGAATCTCCGTCGCTCGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 180
QY 284 TCCGGCGATAAACCCTGGTCAAGATCCTTGATCGATATGGGAAACAGCATGCTGATGATCTT 343
DB 181 TCCGGTGACGACATTTCCAGAAAGAAATTCGAGATCAAGCGAATTCGAGAACAAAAGTAGCCGACAA 60
QY 344 AAAGCCTTGGATCATCAGTCAAAAGCTCTGAACTATGTTTCACTATGAGCTTACTTGAA 403
DB 241 AGAGCCTTAGATCTTGAGAAAAAATTCAGAAATTAATCTCCACACAAAGGATTTACTAGAA 300
QY 404 CTTTGGATAGCAAGCTTTGTTGGGATCAATGTCAAAATATGTGAGTATCGATGCTTTGTT 463
DB 301 ACAGTCCAAAGCAAGCTTTGAAGAACAAATGTCGATATGTAAGTGTAGATCTCTTAAT 360
QY 464 CAACTGGAGGAACACCTTGAGACTCCCTCTCCGTCGTCGTCGTCGTCGTCGTCGTCGTC 523
DB 361 TCTCTGGAGGACAACTTGGAGACTGCTCTGTCGTAAGTAGACTAGGAGGCGAAGCTG 420
QY 524 ATGTTGAAGCTTTGAGAAATCTTAAAGAAAGGAGAAATGCTGAAAGAAAGGAGAACCA 583
DB 421 ATGATGGAGTATATCGAGTCCCTTAAAGAAAGGAGAAATTCCTGAGAGAGAGAACCA 480
QY 584 GTTTTGGCTAGCCAGATGGAGAAATTAATCATATGTGGGAGCAGAAAGCTGAGATGGAGATG 643
DB 481 GTTCTGGCTAGCCAGATGGAGAAAGAAATAGTGTGTCGGCAACAGATGATGAGAGAGAA 540
QY 644 TCACCTGCTGGNCAATCTCCGACAACTCTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 703
DB 541 TTTCCGGGAAGTAGCTCCGGCAACAAATACCGGAGACTCTCCGCTGCTCAATTAGCCA 600
QY 704 CCTTAA 709
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Db          601 CCATCA 606
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CA781283   673 bp mRNA linear EST 03-DEC-2002
LOCUS      014D08AP Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA
DEFINITION
sequence.
ACCESSION  CA781283
VERSION     CA781283.1 GI:26019309
KEYWORDS   EST.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 673)
Lundsgaard, M., Emmersen, J., Nielsen, K.L., Wilson, I., Somerville, S.
and Wellinder, K.G.
EST sequencing of Erysiphe cichoracearum infected Arabidopsis
plants
Unpublished (2002)
Contact: Karen G. Wellinder
Institut for bioteknologi
Aalborg Universitet
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk.
Location/Qualifiers
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/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
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/clone_lib="Infected Arabidopsis Leaf"
/notes="Organ: Leaf; Vector: pBluescript; Mixed cDNA
library of Arabidopsis and E. cichoracearum infected leaf
from three weeks old Arabidopsis plants. Plants were
harvested 3 days after infection and mRNA oligo dT
selected."

FEATURES
source
Query Match 38.5%; Score 362.8; DB 4; Length 673;
Best Local Similarity 75.4%; Pred. No. 2.1e-82;
Matches 451; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 112 GGAAGAGAAAAAAGTAAATCAAGCGAATTGAGAACAAAGTAGCCGACAAAGTCACCTT 171
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Db 63 GTGAAGAGAAAAAATCGAGATCAAGCGAATCGAGAACAAAGCAGTCGACAGTCACCTT 122
|
|
|
QY 172 CTCACAAAGTCGCAACGGTCTCATCGAAGAGCTCGTCAGCTTCTGTTCTCTGTGACGC 231
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Db 123 CTCACAAAGCAGCAATGGTCTCATCGAAGAGCTCGCAACATTCGATTCTGTGAAATC 182
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|
QY 232 ATCCGTGCGCTTCTCTGCTGCTCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCCGCGA 291
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Db 183 CTCGTGCGCTTGTGCTGCTGCTATCGCTCCGGAAGCTCTATGACTTCTCTCCGCTGA 242
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QY 292 TAACCTGGTCAGATCTTGATCGATATGGAAACAGCATGCTGATGATCTTAAAGCCTT 351
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|
Db 243 CGACATTTCCAGATCATTTGATCGTTATGAAATACAAATGCTGATGAACTTAGAGCCTT 302
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|
|
QY 352 GGATCATCACTCAAAAGCTCTGAACATGTTTCACTATGAGTACTTCAACTTGTGA 411
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|
|
Db 303 AGATCTTGAGAAAAAATTCAGAAATATCTTCCACACAGAGATTTACTAGAAAGTCCA 362
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QY 412 TAGCAAGCTTGTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTCAACTGGA 471
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QY 472 GGAACACCTTGAGACTGCCCTCTCCGTGACTAGAGCCAGAGACCGAATCATGTTGAA 531
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Db 423 GGAACAACTTGAGACTGCTCTGTCGTAAGTAGAGCTAGGAAGCGACAACTGATGATGA 482
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QY 532 GCTTTGTTGAGAACTTAAAGAGAGAGAAATCTCGAAAGAGAGAACCAAGGTTTTCGGC 591
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Db 483 GTATATCGATGCTTAAAGAGAGAGAAATTTGCTGAGAGAGAGAACCAAGGTTTTCGGC 542
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|
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|
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Db 543 TAGCCAGATCGGAGAAATATCATGTGCTGGCAACAGATGATGAGAGAGAAATGTTTTCGGG 602
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|
|
QY 652 TGGACAAATCTCCGCAATCTTCGGTGACTCTCCCACTACTTAATTTAGCCACTTAA 709
|
|
|
Db 603 AAGTAGTCCGGCAACAAATATCCGGAGACTCTCCCGCTGCTCAATTTAGCCACCATCA 660
|
|
|
RESULT 13
LOCUS      DR751518
DEFINITION 02-L020098-065-001-B01-Sela MPI2-ADIS-065d Arabidopsis thaliana
cDNA clone 001-B01, mRNA sequence.
ACCESSION  DR751518
VERSION     DR751518.1 GI:71036858
KEYWORDS   EST.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 936)
Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B.,
Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R.,
Coupuland, G., Martin, C., Angenent, G.C., Baumelein, H., Mock, H.P.,
Carbonero, P., Colombo, L., Tonelli, C., Engstrom, P.,
Droge-Laser, W., Gatz, C., Kavanagh, T., Kuehnir, S., Zabeau, M.,
Laux, T., Hordsworth, M., Ruberti, F., Ratcliff, F., Smeekens, S.,
Somschik, I., Weishaar, B. and Traas, J.
REGIA, an EU project on functional genomics of transcription
factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002)
Contact: Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski,
Coupuland, Martin, Angenent, Baumelein, Carbonero, Colombo, Tonelli,
Engstrom, Droge-Laser, Gatz, Kavanagh, Kuehnir, Zabeau, Laux, Hordsworth
Ruberti, Smeekens, Somschik, Weishaar, Traas
Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Email: bernd.weishaar@uni-bielefeld.de
AGI: ATSG65050; SeqAnalysis: structure problem; Translation: no
full cds detected
Data analysis performed in the frame of REGULATORS (Exploiting
inter-species conservation in promoter sequences to identify
regulators of reproductive development and physiological
performance), a Trilateral Co-Operation in Plant Genomics between
Spain (MCYT), France (GENOPLANTS) and Germany (GABI) coordinated by
G. Coupuland (coupuland-mpiz-koeln.mpg.de). Authors: Vincent
Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and
Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE,
lecharny-ad-ibp.u-psud.fr).
Definition of the terms used to describe the quality of the clone:
The about 2250 sequences from the clone collection were sorted
according to clones and clustered. If more than one contig was
formed, the clone was designated 'Contamination'. The contigs and
singletons were blasted against CDS plus pseudogenes from the
TIGR5 annotation, and the resulting AGI code is presented if more
than 90 percent identity was found. The sequences were also blasted
against all TIGR5 introns, and matches longer than 50 bp with 95
percent identity are reported as 'intron found'. The remaining
terms for SeqAnalysis describe the outcome of the evaluation of the
CDS detected after pairwise alignment with CDS plus pseudogenes
from the TIGR5 annotation file. The sequences or contigs for which
a full CDS with or without STOP codon was detected, a BLASTp

```

against all TIGRv5 protein sequences was performed. Full perfect: 100 percent identity; full good: better than 95 percent identity over more than 95 percent of the sequence; partial good: better than 95 percent identity over less than 95 percent of the sequence; weak similarity: less than 95 percent identity over less than 95 percent of the sequence; no similarity: no hit from BLASTp. Note that the collection contains a few clones for which sequencing was not successful, which could have simple technical reasons. Obviously, information about these clones is missing in the submitted data.

Insert Length: 936 Std Error: 0.00

Seq primer: Seta TCGGTTAACTGCTAGCATGGATCTC.

FEATURES

source

Location/Qualifiers
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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="GABI:1450302"
/db_xref="taxon:3702"
/clone="001-B01"
/lab_host="E. coli DH5alpha"
/clone_lib="MPI2-ADIS-065d"
/note="Vector: pDONR201; In the context of the EU-funded Project REGIA (QLG-CT11999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag):
5pr-AATTCGCAATCCCGGATC-3pr; RG_tag2:
5pr-CATGCGCAATCCCGGATC-3pr. During the lifetime of the project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS; head: Bernd Weishaar), the plasmids were re-transformed into DH5alpha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GabipD (<http://gabi.rzpd.de>)."

ORIGIN

Query Match 36.6%; Score 345.2; DB 10; Length 936;
Best Local Similarity 73.6%; Pred. NO. 7.9e-78;
Matches 440; Conservative 0; Mismatches 158; Indels 0; Gaps 0;
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QY 222 TCTGTGACCGATCGCGTCTTCTGTCGTCTTCGCGCTTCGCGCTTCGCGCAAGCTCTACAGCTTCT 281
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DB 264 CTTCCGGTGACCAATGTCAAAGATCATTTGATCGTTTACGAAATATCATCATGCTGATGAC 323
QY 342 TTAAGACCTTGGATCATCAGTCAAAAGCTCTGAACTATGTTTCACTATGAGTACTTTC 401
DB 324 TTGAAGCCTTAGATCTTCGAGAAAAAATCGGAATTTCTGCCATCTCAAGAGTTACTAG 383
QY 402 AACTTGTGATAGCAAGCTTTGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTCG 461

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QY 522 TCATGTTGAAGCTTGTGTTGAGAAATCTTAAAGAAAAGGAGAAAATGCTGAAAAGAGAGAAC 581
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RESULT 14

DR751519/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

DR751519 896 bp mRNA linear EST 19-JUL-2005
02-L020099-065-001-B01-SeLB MP12-ADIS-065d Arabidopsis thaliana
cDNA clone 001-B01, mRNA sequence.
DR751519

DR751519.1 GI:71036859

EST

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 896)

Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B.,

Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R.,

Coupland, G., Martin, C., Angenent, G. C., Baumeister, H., Mock, H. P.,

Carbonero, P., Colombo, L., Tonelli, C., Engstrom, P.,

Droge-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M.,

Laux, T., Hordworth, M., Ruberti, I., Ratcliff, F., Smeekens, S.,

Somsich, I., Weishaar, B. and Traas, J.

REGIA, an EU project on functional genomics of transcription

factors from Arabidopsis thaliana

Comp. Funct. Genomics 3 (2), 102-108 (2002)

Contact:

Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sabl

owski, Coupland, Martin, Angenent, Baumeister, Carbonero, Colombo, Tonelli,

Engstrom, Droge-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Hordworth,

Ruberti, Smeekens, Somsich, Weishaar, Traas

Bielefeld University, Institute for Genome Research

Universitaetstrasse 25, D-33594 Bielefeld, Germany

Email: bernd.weishaar@uni-bielefeld.de

AGI: AT5G5050; SeqAnalysis: structure problem; Translation: no

full cds detected

Data analysis performed in the frame of REGULATORS (Exploiting

inter-species conservation in promoter sequences to identify

regulators of reproductive development and physiological

performance), a Trilateral Co-Operation in Plant Genomics between

Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by

G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent

Thareau (thareau-umr8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and

Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE,

lecharny-ad-ibp.u-psud.fr).

Definition of the terms used to describe the quality of the clone:

The about 2250 sequences from the clone collection were sorted

according to clones and clustered. If more than one contig was

formed, the clone was designated 'Contamination'. The contigs and

singlets were blasted against CDS plus pseudogenes from the

TIGRv5 annotation, and the resulting AGI code is presented if more

than 90 percent identity was found. The sequences were also blasted

against all TIGRv5 introns, and matches longer than 50 bp with 95

percent identity are reported as 'intron found'. The remaining

terms for SeqAnalysis describe the outcome of the evaluation of the

CDS detected after pairwise alignment with CDS plus pseudogenes

102	GGAAGCATTGGAGAAATAAACTAGAAATCAAGCGAATTGAGAACAAAGTAGCGCAG	161
691	GCGAATTCATGGGTAGAAAAAAGTCGAGATCAAGCGAATCGAGAACAAAGTAGTCGAC	632
162	AAGTCACCTCTTCCAAACGTCGGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTC	221
631	AAGTCACCTTTCTCCAAACGACGAATGGTCTCATCGAGAAAGCTCGACACATTTCAATTC	572
222	TCTGTGACGAATCGGTGGCTCTTCTGTGTCTTCGGCTCCGGCAAGCTCTCAAGCTTCT	281
571	TCTGTGAATCTTCCATCGCTGTCTTCGTGTCTTCGGCTCCGGAAACCTCTACAAGTCGT	512
282	CCTCGGGCGATAACTGTGTCAAGATCCTTGATCGATATGGAAACAGCATGCTGATGATC	341
511	CCTCGGTGACACATGTCAAAGATCAATTGATGTTACGAATATCATCATGCTGATGAC	452
342	TTAAGCCTTGGATCATCGATCAAAAGCTCGAACTATGGTTCACTATGAGCTACTTGT	401
451	TTGAAGCCTTAGATCTTGCAGAAAAAATCGGAATTTATCTGCCACTCAAGAAGTTACTAG	392

ORIGIN	deaturase, and CAB (LHCP). "									
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	Best Local Similarity	77.5%;	Pred. No. 4.2e-76;							
	Matches 423;	Conservative	0;	Mismatches 121;	Indels 2;	Gaps 1;				
Qy	65	ACCTGAGATCAAAATTATGGGCACAAAGCCCTCTCGGA--GAGAAAGCCATGGAGAAAGAAA	122							
Db	86	ACATCAGACTCAAAATTATGGGCATAAAGCCCTTGTGCGAAGACGAGCCATGGGGAGAGAA	145							
Qy	123	AACTAGAAATCAAGCGAATTGAGAACACAAAGTAGCCGACACAGTCACCTTCTCCAAACGTC	182							
Db	146	AAGTAGAGATCAAACTAATTAGAAACAAAGTAGTAGCAAGTCACCTTCTCTTAAACGAC	205							
Qy	183	GCAACGGTCTCATCGAGAAAGCTCGTCAGAGCTTTTCTGTTCTCTGTGACGCATCCGTCGCTC	242							
Db	206	GCACTGGTCTCATCGAGAAAGCTCGACAGCTTTTCACTTCTGTGTGATCATCCGTCGCTG	265							
Qy	243	TTCTCGTCGTCGCGCTCCGCGCAAGCTCTACAGCTTCTCTCCGCGGATCAACTGGTCA	302							
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Qy	363	CAAAAGCTCTGAACATATGGTTTCAACATATGAGCTACTTGAACCTTGTGGATAGCAAGCTTG	422							
Db	386	AAAAAAGCTCGGAGTTATCTTCCACAAATGAGTTACTCGAATCAGTCATAAAGCAATCTTG	445							
Qy	423	TGGGATCAAAATGTCAAAAATGTGAGTATCGATGCTCTTGTGTTCAACTGGAGGAAACACCTTG	482							
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Qy	483	AGACTGCGCTCTCCGTGACTAGAGCCCAAGACCGAACTCATGTTTGAAGCTTTGTTGAGA	542							
Db	506	AAACTGCTCTGTCTGCAACTAGAGCTAGGAAGACAGAACTAACGATGGAGTTTGTGGAAGA	565							
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Search completed: May 22, 2006, 08:17:47
Job time : 4487 secs

Job time : 4487 secs

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QY 470 GAGGAACACCTTCAGACTGCCCTCTCCGTGACTAGAGCCCAAGAGCCGAACTCATGTTG 529
Db 361 GAGGAACACCTTCAGACTGCCCTCTCCGTGACTAGAGCCCAAGAGCCGAACTCATGTTG 420
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QY 590 GCTAGCCAGATGAGAAATATCATCATGTGGGAGCAGAACTGAGATGGAGATGTCACCT 649
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QY 830 AAGACTTGTGATGATCTTAAAGTACGAACTAAGTACGAACTAAGTACGAACTAAGTACG 889
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QY 890 AAAAA 895
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RESULT 2
US-09-513-775B-9
; Sequence 9, Application US/09513775B
; Patent No. 6693228
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard
; APPLICANT: Schomburg, Fritz
; APPLICANT: Michaels, Scott
; APPLICANT: Sung, Si-Bum
; TITLE OF INVENTION: Alteration of Flowering Time in Plants
; FILE REFERENCE: 960296.96871
; CURRENT APPLICATION NUMBER: US/09/513,775B
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/121,572
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 60/123,455
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Brassica rapa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(588)
US-09-513-775B-9
Query Match 47.6%; Score 448.6; DB 3; Length 867;
Best Local Similarity 84.2%; Pred. No. 2.1e-116;

Matches 543; Conservative 0; Mismatches 94; Indels 8; Gaps 3;
QY 110 ATGGGAAGAAAAAATCTAGAAATCAAGCGAATTTGAGAAACAAAGTAGCCGACAAAGTCACC 169
Db 1 ATGGGAAGAAAAAATCTAGAAATCAAGCGAATTTGAGAAACAAAGTAGCCGACAAAGTCACC 60
QY 170 TTCTCCAAACGTCGCAACGGTCTCATCGAAGAGCTCGTCAGCTTTCTGTCTCTGTGAC 229
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QY 410 GATAGCAAGCTTGTGGGATCAAAATGTCMAAAATGTGAGTATCGATGCTCTTGTTCACACTG 469
Db 301 GAAAGCAAGCTTGTGGAATCAATTG---ATGATGTAAGCGTGGATTTCCCTCGTTGAGCTA 357
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Db 358 GAAGATCACTTGAAGCTGCGCTCTCTCTGTAAGCTGCGGAGGCGAAGCTTAAATGTTA 417
QY 530 AAGCTTGTGGAATCTTAAAGAAAAGGAGAAAATGCTGAAAAGAGAGAACCCAGGTTTTG 589
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QY 590 GCTAGCCAGATGAGAAATATCATCATGTGGGAGCAGAACTGAGATGGAGATGTCACCT 649
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QY 707 TAAATCGCGGTTGAAATCAAAATCAAAATCAAAATCAATATATTAATGA 751
Db 598 TTACTCGCGGTT--ATCAAAATTAAGAAACATATAATCTAAGA 640

RESULT 3
US-09-513-775B-7
; Sequence 7, Application US/09513775B
; Patent No. 6693228
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard
; APPLICANT: Schomburg, Fritz
; APPLICANT: Michaels, Scott
; APPLICANT: Sung, Si-Bum
; TITLE OF INVENTION: Alteration of Flowering Time in Plants
; FILE REFERENCE: 960296.96871
; CURRENT APPLICATION NUMBER: US/09/513,775B
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/121,572
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 60/123,455
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 863
; TYPE: DNA
; ORGANISM: Brassica rapa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(588)

NAME/KEY: unsure
LOCATION: (839)
OTHER INFORMATION: unsure
US-09-513-775B-7

Query Match 46.6%; Score 439; DB 3; Length 863;
Best Local Similarity 83.3%; Pred. No. 1.1e-113;
Matches 537; Conservative 0; Mismatches 100; Indels 8; Gaps 3;

QY 110 ATGGGAGAAAAAATCTAGAAATCAAGCGAATTGAGAAACAAAGTAGCGGCAAGTCAACC 169
Db 1 ATGGGAGAAAAAATCTAGAAATCAAGCGAATTGAGAAACAAAGTAGCGGCAAGTCAACC 60
QY 170 TTCTCCAAACCTCCGACGGCTCTCATCGAAGAGCTCTGTCAGCTTCTGTTCTCTGTGAC 229
Db 61 TCCTGCAACAGCAGCAAGGGTCTCATCGAAGAGCTCTGTCAGCTTCTGTTCTCTGTGAG 120
QY 230 GCATCCGTCGCTCTTCTGCTGCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 289
Db 121 GCATCTGTTGGCTTCTGTTGCTCTCGCTCCGCAAACTCTACAGCTTCTCTCCGG 180
QY 290 GATAACCTGGTCAAGATCTTGTGATCGATATGGGAAACAGCATGCTGATGATCTCAATGCC 349
Db 181 GATAGACTGGAGAGATCTTGTGATCGATATGGGAAACAAATGCTGATGATCTCAATGCC 240
QY 350 TTGGATCATCATGATCAAGCTCTGAACTATGCTGTTTCACTATGAGCTACTTGAACCTTGTG 409
Db 241 CTGGATCTTCACTCAAACTCTGAACTATGATTTTCACTATGAGCTACTTGAACCTTGTG 300
QY 410 GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTTGTGTTCAACTG 469
Db 301 GAAAGCAAGCTTGTGGATCAATG--ATGATGTAGCGTGGATTCCTCGTTGAGCTA 357
QY 470 GAGGAAACCTTGTGAGACTGCCCTCTCCGTGATAGAGCCAAAGAGCCGAACCTCATGTTG 529
Db 358 GAAGATCACTTGTGAGACTGCCCTCTCTGTAAGTGTGAGCTGCGAAGGAGCAACTAATGTA 417
QY 530 AAGCTTGTGAGATCTTAAAGAAAGAGAAATGCTGAAAGAGAGAACCGAGTTTGTG 589
Db 418 AAGCTTGTGAGATCTTAAAGAAAGAGAAATGCTGTAAGAGAGAGAACCGAGTTTGTG 477
QY 590 GCTAGCCAGATGAGAGATAATCATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACCT 649
Db 478 GCTAGTCAGATGAGAGAGAAATCTTGGAGGAGCCGAGCTGATATATAGATGTCA 537
QY 650 GCTGGAACAATCTCCGA---CAATCTCCGTTGACTCTCCCACTAATTAAATTAGCCACCT 706
Db 538 TCTGGAACAATCTCCGACATCAATCTTCTGTAATCTCTCCGCTGCTTAAATTAACCACT 597
QY 707 TAAATCCGCGTTGAAATCAAAATCCAAACATATATATGA 751
Db 598 TTAATCCGCGGTT--AATCAAAATGAAGAACATATATATCAAGA 640

RESULT 4

US-09-853-450-39
Sequence 39, Application US/09853450
Patent No. 6828478
GENERAL INFORMATION:
APPLICANT: Vanofsky, Martin P.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 687
TYPE: DNA

ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(687)
OTHER INFORMATION: AGL27
US-09-853-450-39

Query Match 34.4%; Score 324.4; DB 3; Length 687;
Best Local Similarity 77.3%; Pred. No. 2.2e-81;
Matches 394; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 110 ATGGGAGAAAAAATCTAGAAATCAAGCGAATTGAGAAACAAAGTAGCGGCAAGTCAACC 169
Db 1 ATGGGAGAAAAAATCTAGAAATCAAGCGAATTGAGAAACAAAGTAGCGGCAAGTCAACC 60
QY 170 TTCTCCAAACCTCCGACGGCTCTCATCGAAGAGCTCTGTCAGCTTCTGTTCTCTGTGAC 229
Db 61 TTCTCCAAACAGCAGCAAGGGTCTCATCGAAGAGCTCTGTCAGCAACTTTCGATTTCTGTGAA 120
QY 230 GCATCCGTCGCTTCTGCTGCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 289
Db 121 TCCTCCGTCGCTTCTGCTGCTCTGCTCCGCAAACTCTATGACTCTTCTCCGGT 180
QY 290 GATAACCTGGTCAAGATCTTGTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCC 349
Db 181 GAGGACATTTTCAAGATCATTTGATCGTATGAAATACACATGCTGATGAACTTAGAGCC 240
QY 350 TTGGATCATCATGCTCAAAAGCTCTGAACTATGTTTCACTATGAGCTACTTGAACCTTGTG 409
Db 241 TTAGATCTTGAAGAAATTCAGATTTCTTCCACACAGGAGTTACTAGAAACAGTC 300
QY 410 GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTTGTGTTCAACTG 469
Db 301 CAAAGCAAGCTTGAAGAAACAAATGTGTAATGTAGTGTAGATTTCTTAATTTCTCTG 360
QY 470 GAGGACACCTTGTGAGACTGCCCTCTCCGTGATAGAGCCAAAGAGCCGAACCTCATGTTG 529
Db 361 GAGGACAACTTGTGAGACTGCTCTGTCGTAAGTAGAGCTAGGAGGAGCAAGTGTATG 420
QY 530 AAGCTTGTGAGAAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAAATGCTGAGAGAGAGAACCGAGTTTGTG 589
Db 421 GAGTATATCGATCCCTTAAAGAAAGGAGAAATGCTGAGAGAGAGAACCGAGTTTGTG 480
QY 590 GCTAGCCAGATGAGAGATAATCATGTTG 619
Db 481 GCTAGCCAGCTGTGAGAGAGAAAGGTATG 510

RESULT 5

US-09-513-775B-3
Sequence 3, Application US/09513775B
Patent No. 6693228
GENERAL INFORMATION:
APPLICANT: Amasino, Richard
APPLICANT: Schomburg, Fritz
APPLICANT: Michaels, Scott
APPLICANT: Sung, Si-Bum
TITLE OF INVENTION: Alteration of Flowering Time in Plants
FILE REFERENCE: 960296.96871
CURRENT APPLICATION NUMBER: US/09/513,775B
CURRENT FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 60/121,572
PRIOR FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: 60/123,455
PRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 907
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS

Qy	170	TTCTCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCCTGTTCTCTGTGAC	229
Db	61	TTCTCAAACGACGCAATGGTCTCATCGACAAGCTCGACAACTTTCGTGAA	120
Qy	230	GCATCCGTCGCTCTTCTCGTGGTCTCCGCTCCGGCAGCTCTACAGCTTCTCTCCCGC	289
Db	121	TCTCCGTCGCTGTTGTTCGTGATCTCGCTCCGAAAACCTATGACCTTCTCTCCGCT	180
Qy	290	GATAACCTGGTCAAGATCCTTGATCGATATGGAAACAGCATGCTGATCATCTTAAAGCC	349
Db	181	GACGAGATAGAAGCGCTGTT-----CAAGCCGAGAAACCTCATGTTTTGAA	228
Qy	350	TTGATCATCATGCTCAAAAGCTCTGAACTATGGTTCACACTATGAGCTACTTGAACCTGTG	409
Db	229	CTCGATCTTTGAAGAAAAAATTCAGAAATTATCTTCACACAAGGAGTTACTAGAAAACGTC	288
Qy	410	GATAGCAGCTTGGGATCAAAATGTCAAAAATGAGTATCGATCGCTCTTGTTTCACTG	469
Db	289	CAAAAGCAAGCTTGAAGAACCAAAATGCGATATGTAAAGTGTAGATTCTCTAAATTTCTCTG	348
Qy	470	GAGGAACAACCTTGAGACGCCCTCTCCGTGACTAGAGCCAGAAGACCGAACTCATGTTG	529
Db	349	GAGGAACAACCTTGAGACTGCTCTGTCGTAAGTAGAGCTAGAGGCGCAACTGATGATG	408
Qy	530	AAGCTTGTGAGAACTCTTAAAGAAAAGGAGAAAATGCTGAAAGAGAGAAACAGAGTTTGTG	589
Db	409	GAGTATATCGAGTCCCTTAAAGAAAAGAGAAAATTGCTTGAGAAAGAGAACCAAGGTTCTG	468
Qy	590	GCTAGCCAGATGGAGAAATAATCATCATCTGGGAGCAGAAGCTGAGATGAGATGTCACCT	649
Db	469	GCTAGCCAGATGGGAAAAGNATACGTTGCTGGCAAACAGATGATGAGAGGAATGTTCCG	528
Qy	650	GCTCGACAATCTCCGACAATCTCCCGTGACTCTCCCACTACTTTAATTAG	700
Db	529	GGAAGTAGCTCCGGCAACAAAATACCGAGACTCTCCCGCTGCTCAATTAG	579

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RESULT 8
US-09-853-450-48
; Sequence 48, Application US/09853450
; Patent No. 6828478
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 7200
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: AGL27 genomic sequence
US-09-853-450-48

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Qy	125	CTAGAAATCAAGCGGAATTGAGACAAAGTAGCCGACGAAGTCACCTTTCTCCAAACGTCGC	184
Db	3016	ATCGAGATCAAGCGGAATCGAGACAAAGCAGTCGACAAGTCACCTTTCTCCAAACGACGC	3075
Qy	185	AACGGTCTCATCGAAGAAAGTCGTACAGCTTTCTGTTCTCTGTGACGATCGGTGCTCTT	244
Db	3076	AATGGTCTCATCGAAGAAAGTCGACAACTTTCGATTCTCTGTGAATCTCTCGGTGCTGT	3135
Qy	245	CTCGTCTGCTCCGGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGA	291
Db	3136	GTCGTGTAATCTGCCTCCGGAAACTATATGACTTCTCTCCGGTGA	3182

RESULT 9
 US-09-869-582-4
 ; Sequence 4, Application US/09869582
 ; Patent No. 6987214
 ; GENERAL INFORMATION:
 ; APPLICANT: Yanofsky, Martin F.
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Methods of Suppressing Flowering in Transgenic Plants
 ; FILE REFERENCE: 19452A-002210US
 ; CURRENT APPLICATION NUMBER: US/09/869,582
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/104,604
 ; PRIOR FILING DATE: 1998-10-16
 ; PRIOR APPLICATION NUMBER: WO PCT/US99/24407
 ; PRIOR FILING DATE: 1999-10-15
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 1294
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; OTHER INFORMATION: AGL2 cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (387)..(1133)
 ; OTHER INFORMATION: AGAMOUS-LIKE 2 (AGL2)
 US-09-869-582-4

Query Match	13.5%	Score	127.6;	DB	4;	Length	1294;
Best Local Similarity	54.4%;	Pred. No.	1.1e-25;				
Matches	296;	Conservative	0;	Mismatches	224;	Indels	24;
						Gaps	1;
Qy	103	AGAAAGCCATGGGAAGAAAAA	ACTAGAAATCAAGCGAAT	TGAGAA	CAAAAGTATGCCGACA	162	
Db	380	AAAAGAANAATGGGAAGAGGA	AGTAGAGCTGGAAGAGAT	TAGAGAA	CAAAATCAACAGACA	439	
Qy	163	AGTCACCTTCTCCAAACGCTG	CGAACGGTCTCATCGAGAAAG	CTCGTCAG	CTTCTCTCTTCT	222	
Db	440	AGTAAAGTTTGAAGAGCGGT	AGGAGACGGTTGTTGAAGAAAG	CTTATGAAT	GTCTCTGTCT	499	
Qy	223	CTGTGACGCATCCGTCGCTCT	TCTCGTCTCCGCTCCGCAAG	CTCTACAGCTTCTC	282		
Db	500	CTGTGATGCTGAAGTTGCTCT	CTCATCATCTTCTCCAACCGT	TGAAAGCTCTATGAGTTTG	559		
Qy	283	CTCCGGGGATAACTGGTCAAG	ATCCTTGATCGATATGGGA	AAACAGCATGCTGATCATCT	342		
Db	560	CAGCTCCTCAAAATGCTCAAG	ACACTTGTATCGGTACCAAGAA	TGCAGCTATGGATCCAT	619		
Qy	343	TAAAGCCTTGGATCATCATGTC	CAAAAG-----CTCTGAAC	CTA	378		
Db	620	TGAAGTCAACAACAACAAAC	CTGCCAAAGAACTTGAGAA	CAGCTACAGAAATATCTGA	679		
Qy	379	TGTTTCACTATGAGCTACTTGA	ACTTTGTGGATAGCAAGCTT	TGGGATCAAAATGTCAA	438		
Db	680	TAAAGGTAGATATGAAACCTT	CAAGCTCAACAGAGAAATCT	TTCTTGGGGAGGATTTAGG	739		
Qy	439	AAATGTGAGTATCGATGCTCTT	GTGTTCAACTGGAGGAAAC	CTTGAAGACTGCCCTCTCCGT	498		

Db 740 ACCTTTGAATTCAAAGGAGTTAGACGAGCTTGAGCGCTCAACTGGACGGCTCTCTCAAGCA 799
QY 499 GACTAGAGCCAAAGAACCGAATCATGTTGTAAGCTTTGTTGAGAACTCTTAAAGAAAGGA 558
Db 800 AGTTCGGTCCATCAAGACACAGTACATGCTTGACCACTCTCGGATCTTCAAAATAAGA 859
QY 559 GAAATGCTGAAGAGAGAACCAAGGTTTTGGCTAGCCAGATGGAGAAATATCATCATGT 618
Db 860 GCAATGTTGTTGAACCAATAGAGCTTTGGCAATGAAGCTGGATGATATGATGTTGT 919
QY 619 GGGG 622
Db 920 GAGA 923

RESULT 10

US-09-869-582-16
; Sequence 16, Application US/09869582
; Patent No. 6987214
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods of Suppressing Flowering in Transgenic Plants
; FILE REFERENCE: 19452A-002210US
; CURRENT APPLICATION NUMBER: US/09/869,582
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 1998-10-16
; PRIOR FILING DATE: 1998-10-16
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1303
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: AGL2 cDNA
; NAME/KEY: CDS
; LOCATION: (396)..(1142)
; OTHER INFORMATION: AGL2
US-09-869-582-16

Query Match 13.5%; Score 127.6; DB 4; Length 1303;
Best Local Similarity 54.4%; Pred. No. 1.1e-25;
Matches 296; Conservative 0; Mismatches 224; Indels 24; Gaps 1;
QY 103 AGAAGCCATGGGAAGAAAAAATCTAGAAATCAAGCGAATTGAGAACAAAGTAGCCGACA 162
Db 389 AAAAGAAATGGGAAGGAGAGTAGAGCTGAAGAGGATAGAGAACAAATCAACAGACA 448
QY 163 AGTCACTTCTCAAGAGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCT 222
Db 449 AGTAACGTTTGCAGAGCGTAGGAACGGTTTGTGGAAGAAAGCTTATGAATTTGCTGTTCT 508
QY 223 CTGTGAGCATCGTCT 282
Db 509 CTGTGAGTGTGAAGTGTCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 568
QY 283 CTCGGCGATPAAGCTGGTCAAGATCTCTGTATCATATGGGAAACAGCATGCTGATGATCT 342
Db 569 CAGCTCTCAACATGCTCAAGACATTTGATCGGTACCAAGAAATGACGATGATGATGATGAT 628
QY 343 TAAAGCTTTGGATCATCAGTCAAAAG-----CTCTGAACTA 378
Db 629 TGAAGTCAACAAACAACTGCGCAAGAACTTTGAGAACAGCTACAGAGAAATATCTGAAGCT 688
QY 379 TGGTTACACATATGAGTACTTCAACTTGTGGATAGCAAGCTTGTGGATCAAAATCTCAA 438
Db 689 TAAGGGTAGNATAGAGAACCTTCAACGTCAACAGAGAAATCTTCTTTGGGAGGATTTAGG 748
QY 439 AAATGTGATATCGATGCTCTTGTTCAACTGGAGGAACCTTTGAGACTGCCCTCTCTCCGT 998

Db 749 ACCTTTGAATTCAAAGGAGTTAGACGAGCTTGAGCGCTCAACTGGACGGCTCTCTCAAGCA 808
QY 499 GACTAGAGCCAAAGAACCGAATCATGTTGTAAGCTTTGTTGAGAACTCTTAAAGAAAGGA 558
Db 809 AGTTCGGTCCATCAAGACACAGTACATGCTTGACCACTCTCGGATCTTCAAAATAAGA 868
QY 559 GAAATGCTGAAGAGAGAACCAAGGTTTTGGCTAGCCAGATGGAGAAATATCATCATGT 618
Db 869 GCAATGTTGTTGAACCAATAGAGCTTTGGCAATGAAGCTGGATGATATGATGTTGT 928
QY 619 GGGG 622
Db 929 GAGA 932

RESULT 11

US-09-853-450-27
; Sequence 27, Application US/09853450
; Patent No. 6828478
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(747)
; OTHER INFORMATION: SEPALLATA1 (SEP1)
US-09-853-450-27

Query Match 13.3%; Score 125.4; DB 3; Length 747;
Best Local Similarity 54.4%; Pred. No. 3.5e-25;
Matches 292; Conservative 0; Mismatches 221; Indels 24; Gaps 1;
QY 110 ATGGGAAGAAAAAATCTAGAAATCAAGCGAATTGAGAACAAAGTAGCCGACCAAGTACC 169
Db 1 ATGGGAAGAGGAAGAGTAGAGCTGAAGAGGATAGAGAACAAATCAACAGACAAAGTAACG 60
QY 170 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTCTCTCTGAC 229
Db 61 TTGCAAAAGCGTAGGAACGGTTTGTGGAAGAAAGCTTATGAATTTGCTCTCTCTGAT 120
QY 230 GCATCGCTCGCT 289
Db 121 GTTGAAGTGTCTCTCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 290 GATAACCTGGTCAAGATCTTGTATGATATGGAAACAGCATGCTGATGATGATCTTAAAGCC 349
Db 181 TCAAAACATGCTCAAGACACTTGTATCGGTACCAAGAAATGCGATGATGATGATGATGAT 240
QY 350 TTGGATCATCAGTCAAAAG-----CTCTGAACTATGTTCA 385
Db 241 AACCAAAACCTGCGCAAGAACTTGGATAGCAAGCTTTGGGATCAAAATCTCAAAATGTTG 300
QY 386 CACTATGAGCTACTTGAACCTTGTGGATAGCAAGCTTTGGGATCAAAATCTCAAAATGTTG 445
Db 301 AGATATGAGAACCTTCAAGCTCAACAGAGAAATCTTCTTTGGGAGGATTTAGGACCTTTG 360
QY 446 AGTATCGATGCTTGTGTTCAACTGGAGGAACACCTTTGAGACTGCGCTCTCTCCGTGACTAG 505
Db 361 AATTCAAAGGAGTTAGAGCAGCTTGTAGCGTCAACTGGACGGCTCTCTCTCAAGCAAGTTCCG 420

Db 733 GCCTCAACTAGACGGCTCTCTGAAGCAAGTTGCTGCATCAAGACACAGTATATGCTTGA 792
Qy 532 GCTTGTGAGAACTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACCGAGTTTGGC 591
Db 793 CCAGCTCTCTGATCTTCAAGGTAAAGGAGCATATCTTGTCTTGAATGCCAACACAGAGCTTTGTC 852
Qy 592 TAGCCAGATCGAGAATA 608
Db 853 AATGAAGCTGGAAGATA 869

RESULT 14

US-09-853-450-29
; Sequence 29, Application US/09853450
; Patent No. 6828478
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Gary
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-00240005
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(753)
; OTHER INFORMATION: SBPALLATA2 (SBP2)
US-09-853-450-29

Query Match 12.7%; Score 119.4; DB 3; Length 753;
Best Local Similarity 54.1%; Pred. No. 1.7e-23;
Matches 283; Conservative 0; Mismatches 216; Indels 24; Gaps 1;
Qy 110 ATGGGAAGAAAAAAGCTAGAAATCAAGCGAATTTAGAAACAAAAGTAGCCGACAAAGTCACC 169
Db 1 ATGGGAAGAGGAAGAGTAGAGCTCAAGAGGATAGAGAACAAATCAACAGACAGAGTGACG 60
Qy 170 TTCTCAGAAAGCTCGAACGGTCTATCGAGAAAGCTGTCAGCTTTCTGTTCTCTGTGAC 229
Db 61 TTGTCTAAACGTAGAAATGTTTGTCTGAAAAAAGCTTATGAGCTTTCTGTTCTCTGCGAT 120
Qy 230 GCATCGCTCGCTCTTCTGCTGCTCTCGGCTCCGGCAAGCTCTACAGCTTCTCCTCCGGC 289
Db 121 GCTGAAGTCTCTCATGCTTTCTTCCAAACGTTGGCAAGCTCTACAGTTCCTGACAGACC 180
Qy 290 GATAACCTGGTCAAGATCTTGTATGATATGGGAAACAGCATGCTGATGATCTTAAAGCC 349
Db 181 TCCAAACATGCTCAAGACATCGAAAGGTATCAGAAAGTATCAGAAAGTATGCTCCATTTGAGTC 240
Qy 350 TTGGATCATAGTCAAAAGCTCTGAAGTATGGTT-----CA 385
Db 241 AACAAACAAACCTGTAAGAGCTTGAGAACAGCTACAGAGAGTACTTGAAGCTGAAAGGT 300
Qy 386 CACTATGAGCTACTTGAACCTTGTGGATAGCAAGCTTGTGGGATCAAAATGCAAAATG 445
Db 301 AGATATGAAATCTGCACGTCAGCAGAGAAATCTTCTTGGAGAGATCTTGGACCTCTG 360
Qy 446 AGTATCGATGCTCTTGTTCACATGGAGGAAACCTTGGAGACTGCCCTCTCCGTGACTAGA 505
Db 361 AATTCAAAGAGCTAGAGCAGCTTGAGCGTCACTAGACGGCTCTCTGAAGCAAGTTCCG 420
Qy 506 GCCAAGAACCGAACTCATGTTGAGCTTTGTTGAGAAATCTTAAAGAAAGGAGAAATG 565
Db 421 TGCATCAAGACACAGTATATGCTTGAACCAAGCTCTCTGATCTTCAAGGTAAAGGAGCATATC 480

Qy 566 CTGAAGAGAGAGAACCCAGGTTTTTGGCTAGCCAGATCGAGAATA 608
Db 481 TTGCTTGATGCCAACAGAGCTTTGTCAATGAAGCTGGAAGATA 523
RESULT 15
US-08-592-214A-7
; Sequence 7, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1345
; NAME/KEY: misc feature
; LOCATION: 1..1345
; OTHER INFORMATION: /note= "product = Zea mays API"
US-08-592-214A-7

Query Match 11.8%; Score 111.6; DB 2; Length 1345;
Best Local Similarity 52.6%; Pred. No. 3.7e-21;
Matches 286; Conservative 0; Mismatches 234; Indels 24; Gaps 1;
Qy 105 AAGCATCGGAAGAAAAAACTAGAAATCAAGCGAATTTAGAAACAAAAGTAGCCGACCAAG 164
Db 144 AGGCGATGGGCGCGGCAAGGTACAGCTGMAAGCGATAGAGAACAAAGATAAACCCGCGAG 203
Qy 165 TCACCTTCTCCAAAGCTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCT 224
Db 204 TGACCTTCTCCAAAGCGCGGAAACGGCTCTCAAGAAAGCGCACGAGATCTCCGCTCTCT 263
Qy 225 GTGAGCATCGTCTGCTCTTCTCGTCTGCTCGGCTCCGGCAAGCTCTACAGCTTTCTCTCT 284
Db 264 GCGATCGCGAGGTGCGCGCTCATGCTTCTCTCCCAAGGCGCAGCTCTACGAGTAGCGCA 323
Qy 285 CCGCGGATAACTGCTCAAGATCCCTTGTATCGATATGGGAAACAGCATGCTGATGATCTTGA 344
Db 324 CCGACTCCCGCATGAGCAAAAATTTCTTGAACGCTATGAGCGGATATTCCTATGCTGAAAGG 383

Qy	345	AAGCCTTGGATCATCAGTCGAAAGCTCTGAACTATGGTTCACTA-----	390
Db	384	CTCTTATTTTCAGCTGAATCTGAAAGTGAGGGAAATTTGGTCCCGAATACAGGAACTGA	443
Qy	391	-----TGAGCTACTTGCAACTTTGTGGATAGCAAGCTTGTGGGATCAAAATGTCAAAA	440
Db	444	AGGCCAAATTTGAGACCCATACAAAATGCCAAGCACCTGATGGGAGGATCTAGAGT	503
Qy	441	ATGTGAGTATCGATGCTCTTTGTTCAACTGGAGGAAACACCTTGAGACTGCCCTCTCCGTGA	500
Db	504	CTTTGAATCCCAAAGAGCTCCAGCAACTAGAGCAGCAGCTGATAGCTCACTGAAGCACA	563
Qy	501	CTAGAGCCAGAGAACCGAATCATGTGTGAAGCTTTGTGAGAACTTTAAGAAAAGGAGA	560
Db	564	TCAGATCAAGGAGAGAGCCACCTTATGGCCGAGTCTATTTCTGAGCTACAGAAAGGAGA	623
Qy	561	AAATGCTGMAAGAGAGAACCAAGGTTTTTGGCTAGCCAGATGGAGAAATATCATCATGTGG	620
Db	624	GGTCACTGCAGGAGGAGAACAGGCTCTGCAGAAGGAACTTTCGGAGAGGCGAAGGCCG	683
Qy	621	GAGC 624	
Db	684	TCGC 687	

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OM nucleic - nucleic search, using sw model

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(without alignments)
7813.378 Million cell updates/sec

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Perfect score: 943
Sequence: 1 cggaaagagaaaaaa.....tgagaaaaaa 943

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Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	943	100.0	943	8	US-10-374-780A-2129
3	943	100.0	943	8	US-10-412-699B-1873
4	943	100.0	943	10	US-10-225-066A-767
5	784.4	83.2	797	10	US-10-600-948-1
6	591	62.7	591	10	US-10-905-520-5
7	448.6	47.6	867	10	US-10-600-948-9
8	439	46.6	863	10	US-10-600-948-7
9	373.6	39.5	884	16	US-11-172-740-578
10	372.6	39.5	883	7	US-10-225-066A-1087
11	372.6	39.5	883	8	US-10-374-780A-15
12	372.6	39.5	883	8	US-10-412-699B-69
13	372.6	39.5	883	8	US-10-412-699B-1733
14	372.6	39.5	883	10	US-10-225-066A-1087
15	363.8	38.6	1059	7	US-10-225-066A-1055
16	363.8	38.6	1059	8	US-10-374-780A-349
17	363.8	38.6	1059	8	US-10-412-699B-943

18	363.8	38.6	1059	8	US-10-412-699B-1881
19	363.8	38.6	1059	10	US-10-225-066A-1055
20	362.6	38.5	1036	7	US-10-225-066A-1109
21	362.6	38.5	1036	8	US-10-374-780A-165
22	362.6	38.5	1036	8	US-10-412-699B-567
23	362.6	38.5	1036	8	US-10-412-699B-1811
24	362.6	38.5	1036	10	US-10-225-066A-1109
25	360.6	38.2	604	10	US-10-487-901-1055
C	347	36.8	877	8	US-10-425-114-20176
26	339.6	36.0	610	8	US-10-412-699B-1950
27	339.6	35.7	537	10	US-10-487-901-3369
28	334	35.4	5968	10	US-10-905-520-6
29	324.4	34.4	687	3	US-09-853-450-39
30	324.4	34.4	687	9	US-10-794-923-39
31	324.4	34.4	907	10	US-10-600-948-3
32	324.4	34.4	907	10	US-10-600-948-3
33	319.4	33.9	818	7	US-10-225-066A-383
34	319.4	33.9	818	8	US-10-374-780A-351
35	319.4	33.9	818	8	US-10-412-699B-945
36	319.4	33.9	818	8	US-10-412-699B-1883
37	319.4	33.9	818	10	US-10-225-066A-383
38	317.6	33.7	769	10	US-10-600-948-5
39	311.2	33.0	834	8	US-10-374-780A-2145
40	311.2	33.0	834	8	US-10-412-699B-947
41	311.2	33.0	834	8	US-10-412-699B-1885
42	311.2	33.0	877	16	US-11-172-740-2509
43	297.8	31.6	579	3	US-09-853-450-49
44	297.8	31.6	579	9	US-10-794-923-49
45	297.4	31.5	880	8	US-10-412-699B-1952

ALIGNMENTS

RESULT 1

US-10-225-066A-767
; Sequence 767, Application US/10225066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: REICHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: RUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI0036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 767
; LENGTH: 943
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-767

Query Match		100.0%;	Score 943;	DB 7;	Length 943;
Best Local Similarity		100.0%;	Pred. No. 2.6e-246;		
Matches 943;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CGAGAAAAGGAAAAAATAAGAGAGAAAACGCTTAGTATCTCCGGCGACTTGAAC	60		
DB	1	CGAGAAAAGGAAAAAATAAGAGAGAAAACGCTTAGTATCTCCGGCGACTTGAAC	60		
QY	61	CCAAACCTGAGGATCAAAATTAGGGCCAAAGCCCTCTCGGAGAGAAAGCCATGGGAAGAA	120		
DB	61	CCAAACCTGAGGATCAAAATTAGGGCCAAAGCCCTCTCGGAGAGAAAGCCATGGGAAGAA	120		
QY	121	AAACTAGAAATCAAGGAATTGAGAAACAAAGTAGCCGACAGTCACTTCTTCCAAACG	180		
DB	121	AAACTAGAAATCAAGGAATTGAGAAACAAAGTAGCCGACAGTCACTTCTTCCAAACG	180		
QY	181	TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTCTCTGTGAGCCATCCGTCGC	240		
DB	181	TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTCTCTGTGAGCCATCCGTCGC	240		
QY	241	TCCTCTCGTCTCCGGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATAACCTGGT	300		
DB	241	TCCTCTCGTCTCCGGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATAACCTGGT	300		
QY	301	CAAGATCTTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA	360		
DB	301	CAAGATCTTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA	360		
QY	361	GTCAAGCTCTCAACTATGTTTCACTATGAGCTACTTGAACCTTGTGATAGCAAGCT	420		
DB	361	GTCAAGCTCTCAACTATGTTTCACTATGAGCTACTTGAACCTTGTGATAGCAAGCT	420		
QY	421	TGTGGGATCAAAATGTCAAAATGTAGTATCGATGCTCTTGTTCACCTCGAGGAACACCT	480		
DB	421	TGTGGGATCAAAATGTCAAAATGTAGTATCGATGCTCTTGTTCACCTCGAGGAACACCT	480		
QY	481	TGAGACTCGCCTCTCCGTGACTAGAGCCCAAGAACCGAACTCATGTTGAAGCTTGTGA	540		
DB	481	TGAGACTCGCCTCTCCGTGACTAGAGCCCAAGAACCGAACTCATGTTGAAGCTTGTGA	540		
QY	541	GAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACCGAGTTTGGCTAGCCAGAT	600		
DB	541	GAATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACCGAGTTTGGCTAGCCAGAT	600		
QY	601	CGAGAAATATCATCATGTGGAGCAGAACTGAGATGGAGATGTCACTGTGGCAAAAT	660		
DB	601	CGAGAAATATCATCATGTGGAGCAGAACTGAGATGGAGATGTCACTGTGGCAAAAT	660		
QY	661	CTCCGACAACTTCCGGTGACTCTCCACTACTTAAATAGCCACCTTAAATCGGGGTTG	720		
DB	661	CTCCGACAACTTCCGGTGACTCTCCACTACTTAAATAGCCACCTTAAATCGGGGTTG	720		
QY	721	AAATCAAAATCCAAACATATATTAATGAAGAAAAAATAAGATATGTAATTATT	780		
DB	721	AAATCAAAATCCAAACATATATTAATGAAGAAAAAATAAGATATGTAATTATT	780		
QY	781	CGCTGATAAGGCGAGCGTTTGTATCTTAAATCTCTCTTTGGCCCAAGAGACTTTG	840		
DB	781	CGCTGATAAGGCGAGCGTTTGTATCTTAAATCTCTCTTTGGCCCAAGAGACTTTG	840		
QY	841	TGTGTGATACTTAAAGTAGCGGAACCTAAGTCAATACTATCTGTTTTAAGCAAAAGGTTG	900		
DB	841	TGTGTGATACTTAAAGTAGCGGAACCTAAGTCAATACTATCTGTTTTAAGCAAAAGGTTG	900		
QY	901	ATGAACCTTTGATCTTATTCGTGTGAGAAAAAATAAAAAA	943		
DB	901	ATGAACCTTTGATCTTATTCGTGTGAGAAAAAATAAAAAA	943		

RESULT 2
US-10-374-780A-2129
; Sequence 2129, Application US/10374780A
; Publication No. US20040019927A1

GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
APPLICANT: Creelman, Robert A
APPLICANT: Ratcliffe, Oliver
APPLICANT: Adam, Luc J
APPLICANT: Reuber, T. Lynne
APPLICANT: Keddle, James
APPLICANT: Broun, Pierre E
APPLICANT: Pilgrim, Marsha L
APPLICANT: Dubell III, Arnold T
APPLICANT: Pineda, Omaira
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: Patentin version 3.2
SEQ ID NO 2129
LENGTH: 943
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G1759 Predicted polypeptide sequence is paralogous to G157, G859,
US-10-374-780A-2129

Query Match		100.0%;	Score 943;	DB 8;	Length 943;
Best Local Similarity		100.0%;	Pred. No. 2.6e-246;		
Matches 943;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CGAGAAAAGGAAAAAATAAGAGAGAAAACGCTTAGTATCTCCGGCGACTTGAAC	60		
DB	1	CGAGAAAAGGAAAAAATAAGAGAGAAAACGCTTAGTATCTCCGGCGACTTGAAC	60		
QY	61	CCAAACCTGAGGATCAAAATTAGGGCCAAAGCCCTCTCGGAGAGAAAGCCATGGGAAGAA	120		
DB	61	CCAAACCTGAGGATCAAAATTAGGGCCAAAGCCCTCTCGGAGAGAAAGCCATGGGAAGAA	120		
QY	121	AAACTAGAAATCAAGGAATTGAGAAACAAAGTAGCCGACAGTCACTTCTTCCAAACG	180		
DB	121	AAACTAGAAATCAAGGAATTGAGAAACAAAGTAGCCGACAGTCACTTCTTCCAAACG	180		
QY	181	TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTCTCTGTGAGCGATCCGTCGC	240		
DB	181	TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTCTGTCTCTGTGAGCGATCCGTCGC	240		
QY	241	TCCTCTCGTCTCCGGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATAACCTGGT	300		
DB	241	TCCTCTCGTCTCCGGCTCCGGCAAGCTCTACAGCTTCTCTCCGGCGATAACCTGGT	300		
QY	301	CAAGATCTTTGATCGATATGGGAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA	360		

Db 301 CAAGATCCTTGCATCGATATGGAAACACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA 360
Qy 361 GTCAAAAGCTCTGAACATATGTTTACACTATGAGCTACTTGAACCTTGGATAGCAAGCT 420
Db 361 GTCAAAAGCTCTGAACATATGTTTACACTATGAGCTACTTGAACCTTGGATAGCAAGCT 420
Qy 421 TGTGGGATCAAAATGTCAAAATGTGAGTATGATGATGCTCTTCTTCAACTGGAGGACCACT 480
Db 421 TGTGGGATCAAAATGTCAAAATGTGAGTATGATGATGCTCTTCTTCAACTGGAGGACCACT 480
Qy 481 TGAGACTGCCCTCTCCGCTGACTAGAGCCAAAGACCGAACTCATGTTTGAAGCTTGTGA 540
Db 481 TGAGACTGCCCTCTCCGCTGACTAGAGCCAAAGACCGAACTCATGTTTGAAGCTTGTGA 540
Qy 541 GAATCTTAAAGAAAGGAGAAATGCTGAAGAGAGAGAACCAAGCTTTTGGCTAGCCAGAT 600
Db 541 GAATCTTAAAGAAAGGAGAAATGCTGAAGAGAGAGAACCAAGCTTTTGGCTAGCCAGAT 600
Qy 601 GGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGAGATGTCACCTGCTGACCAAT 660
Db 601 GGAGAAATATCATCATGTGGGAGCAGAGCTGAGATGAGATGTCACCTGCTGACCAAT 660
Qy 661 CTCGCACAATCTTCCGCTGACTCTCCCACTACTTAAATTTAGCCACTTAAATCGCGGTTG 720
Db 661 CTCGCACAATCTTCCGCTGACTCTCCCACTACTTAAATTTAGCCACTTAAATCGCGGTTG 720
Qy 721 AAATCAAAATCCAAACATATATTAATTATGAAGAAAAAATAAGATATGTAATATT 780
Db 721 AAATCAAAATCCAAACATATATTAATTATGAAGAAAAAATAAGATATGTAATATT 780
Qy 781 CCGCTGATAGGGGAGCGGTTTGTATATCTTAAATCTCTCTTCTTGGCCAGAGACTTTG 840
Db 781 CCGCTGATAGGGGAGCGGTTTGTATATCTTAAATCTCTCTTCTTGGCCAGAGACTTTG 840
Qy 841 TGTGTGATCTTAAGTAGAGCGAACTAAGTCAATCTATCTGTTTAAAGACAAAGGTTG 900
Db 841 TGTGTGATCTTAAGTAGAGCGAACTAAGTCAATCTATCTGTTTAAAGACAAAGGTTG 900
Qy 901 ATGAACCTTTGACCTTATTCGTGTGAGAAAAAATAAAAAA 943
Db 901 ATGAACCTTTGACCTTATTCGTGTGAGAAAAAATAAAAAA 943

RESULT 3

US-10-412-699B-1873
; Sequence 1873, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Broun, Pierre E.
; APPLICANT: Pineda, Omaidra
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: Dubell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kumimoto, Roderick
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519

; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142
; PRIOR FILING DATE: 2001-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1873
; LENGTH: 943
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-412-699B-1873

Query Match 100.0%; Score 943; DB 8; Length 943;
Best Local Similarity 100.0%; Pred. No. 2,6e-246;
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAGAAAGGAAAAAATAAGAGAGAAAAAGCTTAGTATCTCGGCGACTTGAAC 60
Db 1 CGAGAAAGGAAAAAATAAGAGAGAAAAAGCTTAGTATCTCGGCGACTTGAAC 60
Qy 61 CCAAACTGAGGATCAAAATTTAGGGCACAAGCCCTCTCGAGAGAGCCATGGAGAA 120
Db 61 CCAAACTGAGGATCAAAATTTAGGGCACAAGCCCTCTCGAGAGAGCCATGGAGAA 120
Qy 121 AAAAATAGAAATCAAGCGAATTTAGAGACAAAGTAGCCGACACTTCTCCAAACG 180
Db 121 AAAAATAGAAATCAAGCGAATTTAGAGACAAAGTAGCCGACACTTCTCCAAACG 180
Qy 181 TCGCAACGGTCTCATCGAGAAAGCTCTGAGCTTTCTGTTCTCTGTGACGATCCGTCG 240
Db 181 TCGCAACGGTCTCATCGAGAAAGCTCTGAGCTTTCTGTTCTCTGTGACGATCCGTCG 240
Qy 241 TCTTCTGCTGCTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCGCGGATACCTGGT 300
Db 241 TCTTCTGCTGCTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCTCCGCGGATACCTGGT 300
Qy 301 CAAGATCCTTGTGATGATGAGAAACAGCATGCTGATGATCTTAAAGCTTTGGATCATCA 360
Db 301 CAAGATCCTTGTGATGATGAGAAACAGCATGCTGATGATCTTAAAGCTTTGGATCATCA 360
Qy 361 GTCAAAAGCTCTGAACATATGTTTCACTATGAGCTACTTGAACCTTGTGGATAGCAAGCT 420
Db 361 GTCAAAAGCTCTGAACATATGTTTCACTATGAGCTACTTGAACCTTGTGGATAGCAAGCT 420
Qy 421 TGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACCTGAGGAGACACT 480
Db 421 TGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACCTGAGGAGACACT 480
Qy 481 TGAGACTGCCCTCTCCGCTGACTAGAGCCAAAGACCGAACTCATGTTTGAAGCTTGTGA 540
Db 481 TGAGACTGCCCTCTCCGCTGACTAGAGCCAAAGACCGAACTCATGTTTGAAGCTTGTGA 540
Qy 541 GAATCTTAAAGAAAGGAGAAATGCTGAAGAGAGAGAACCAAGCTTTTGGCTAGCCAGAT 600
Db 541 GAATCTTAAAGAAAGGAGAAATGCTGAAGAGAGAGAACCAAGCTTTTGGCTAGCCAGAT 600
Qy 601 GGAGAAATATCATCATGTGGGAGCAGAAAGCTGAGATGAGATGTCACCTGCTGACCAAT 660

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Db 601 GGAGAAATTAATCATCATCTGGGAGCAGAGCTGAGATGGAGATGTCACTCTCGACAAAT 660
Qy 661 CTCGCAAACTCTCCGGTGAATCTCCCACTACTTAAATTAAGCAGCTTAAATTCGGCGTTG 720
Db 661 CTCGCAAACTCTCCGGTGAATCTCCCACTACTTAAATTAAGCAGCTTAAATTCGGCGTTG 720
Qy 721 AAATCAAAATCCAAAACATATATAATTAAGAGAAAAAATAAGATATGTAATTAAT 780
Db 721 AAATCAAAATCCAAAACATATATAATTAAGAGAAAAAATAAGATATGTAATTAAT 780
Qy 781 CCGCTGATAAGGGCGAGCGTTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGACTTTG 840
Db 781 CCGCTGATAAGGGCGAGCGTTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGACTTTG 840
Qy 841 TGTGTGATCTTAAGTAGAGCGAAGCTAAGTCAATCTACTCTGTTTAAAGCAAAAGGTTG 900
Db 841 TGTGTGATCTTAAGTAGAGCGAAGCTAAGTCAATCTACTCTGTTTAAAGCAAAAGGTTG 900
Qy 901 ATGAACCTTGTACTTATTCGTGTGAGAAAAAATAAGAAAAA 943
Db 901 ATGAACCTTGTACTTATTCGTGTGAGAAAAAATAAGAAAAA 943
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RESULT 4

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US-10-225-066A-767
; Sequence 767, Application US/10225066A
; Publication No. US20050160493A9
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MB10036-2 US
; CURRENT APPLICATION NUMBER: US/10/225, 066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 767
; LENGTH: 943
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-767
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Query Match 100.0%; Score 943; DB 10; Length 943;
Best Local Similarity 100.0%; Pred. No. 2.6e-246;
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGAGAAACGAAAAAATAAGAGAGAAAAACCTTAGTATCTCCGGCGACTTGAAC 60
Db 1 CGAGAAACGAAAAAATAAGAGAGAAAAACCTTAGTATCTCCGGCGACTTGAAC 60
Qy 61 CCAAACTGAGGATCAAAATTAGGGCAAAAGCCCTCTCGAGAGAGAGCCATCGGAAGAAA 120
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Db 61 CCAAACTGAGGATCAAAATTAGGGCAAAAGCCCTCTCGAGAGAGAGCCATCGGAAGAAA 120
Qy 121 ABAAC TAGAATCAAGCGAATTCAGAACAAAAGTAGCCGACAGTCACTTCTCCAAACG 180
Db 121 ABAAC TAGAATCAAGCGAATTCAGAACAAAAGTAGCCGACAGTCACTTCTCCAAACG 180
Qy 181 TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGACGATCCGTCGC 240
Db 181 TCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGACGATCCGTCGC 240
Qy 241 TCTTCTCGTCTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCCTCCGGCGATAACCTGGT 300
Db 241 TCTTCTCGTCTCTCCGCTCCGCGCAAGCTCTACAGCTTCTCCTCCGGCGATAACCTGGT 300
Qy 301 CAAGATCTCTGATCGATATGGGAAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA 360
Db 301 CAAGATCTCTGATCGATATGGGAAAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCA 360
Qy 361 GTCAAAAGCTCTGAACATATGTTTCAACATATGAGCTACTTGAACCTTGTGGATAGCAAGCT 420
Db 361 GTCAAAAGCTCTGAACATATGTTTCAACATATGAGCTACTTGAACCTTGTGGATAGCAAGCT 420
Qy 421 TGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTGGAGGAACACCT 480
Db 421 TGTGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTGGAGGAACACCT 480
Qy 481 TGAGACTGCCCTCTCCGCTAGACTAGAGCCAAAGAACCGAACTCATGTTGAAGCTTGTGA 540
Db 481 TGAGACTGCCCTCTCCGCTAGACTAGAGCCAAAGAACCGAACTCATGTTGAAGCTTGTGA 540
Qy 541 GAATCTTAAAGAAAAGGAGAAAATGCTGAAAGAGAGAACCCAGGTTTTCGCTAGCCAGAT 600
Db 541 GAATCTTAAAGAAAAGGAGAAAATGCTGAAAGAGAGAACCCAGGTTTTCGCTAGCCAGAT 600
Qy 601 GGAGAAATTAATCATCATCTGGGAGCAGAGCTGAGATGGAGATGTCACTCTCGACAAAT 660
Db 601 GGAGAAATTAATCATCATCTGGGAGCAGAGCTGAGATGGAGATGTCACTCTCGACAAAT 660
Qy 661 CTCGCAAACTCTCCGGTGAATCTCCCACTACTTAAATTAAGCAGCTTAAATTCGGCGTTG 720
Db 661 CTCGCAAACTCTCCGGTGAATCTCCCACTACTTAAATTAAGCAGCTTAAATTCGGCGTTG 720
Qy 721 AAATCAAAATCCAAAACATATATAATTAAGAGAAAAAATAAGATATGTAATTAAT 780
Db 721 AAATCAAAATCCAAAACATATATAATTAAGAGAAAAAATAAGATATGTAATTAAT 780
Qy 781 CCGCTGATAAGGGCGAGCGTTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGACTTTG 840
Db 781 CCGCTGATAAGGGCGAGCGTTTGTATATCTTAATATCTCTCTTTGGCCAAAGAGACTTTG 840
Qy 841 TGTGTGATCTTAAGTAGAGCGAAGCTAAGTCAATCTACTCTGTTTAAAGCAAAAGGTTG 900
Db 841 TGTGTGATCTTAAGTAGAGCGAAGCTAAGTCAATCTACTCTGTTTAAAGCAAAAGGTTG 900
Qy 901 ATGAACCTTGTACTTATTCGTGTGAGAAAAAATAAGAAAAA 943
Db 901 ATGAACCTTGTACTTATTCGTGTGAGAAAAAATAAGAAAAA 943
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RESULT 5

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US-10-600-948-1
; Sequence 1, Application US/10600948
; Publication No. US20050091717A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard
; APPLICANT: Schomburg, Fritz
; APPLICANT: Michaels, Scott
; APPLICANT: Sung, Si-Bum
; TITLE OF INVENTION: Alteration of Flowering Time in Plants
; FILE REFERENCE: 960296.96871
; CURRENT APPLICATION NUMBER: US/10/600,948
; CURRENT FILING DATE: 2003-06-20
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;; PRIOR APPLICATION NUMBER: US/09/513,775
;; PRIOR FILING DATE: 2000-02-25
;; PRIOR APPLICATION NUMBER: 60/121,572
;; PRIOR FILING DATE: 1999-02-25
;; PRIOR APPLICATION NUMBER: 60/123,455
;; PRIOR FILING DATE: 1999-03-05
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 797
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
;; FEATURES:
;; NAME/KEY: CDS
;; LOCATION: (1)..(588)
US-10-600-948-1

Query Match 83.2%; Score 784.4; DB 10; Length 797;
Best Local Similarity 99.9%; Pred. No. 4.8e-203;
Matches 785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 110 ATGGGAAGAAAAAATAGAAATCAAGCGAATTCAGAAACAAAGTAGCCGACAAAGTCAC 169
Db 1 ATGGGAAGAAAAAATAGAAATCAAGCGAATTCAGAAACAAAGTAGCCGACAAAGTCAC 60

Qy 170 TTCTCCAAAGTCGCAAGGCTCTCATCGAAGAACTGTCAGCTTCTGTTCTCTGTGAC 229
Db 61 TTCTCCAAAGTCGCAAGGCTCTCATCGAAGAACTGTCAGCTTCTGTTCTCTGTGAC 120

Qy 230 GCATCCGTCGCTCTTCTGTCGTCCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 289
Db 121 GCATCCGTCGCTCTTCTGTCGTCCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 180

Qy 290 GATAACCTGGTCAAGATCTTGAATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC 349
Db 181 GATAACCTGGTCAAGATCTTGAATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC 240

Qy 350 TTGGATCATCAGTCAGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTGTG 409
Db 241 TTGGATCATCAGTCAGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTGTG 300

Qy 410 GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTG 469
Db 301 GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTG 360

Qy 470 GAGGAAACCTTTGAGACTGCGCTCTCCGTGACTAGAGCCAAAGAGACCGAACTCATGTTG 529
Db 361 GAGGAAACCTTTGAGACTGCGCTCTCCGTGACTAGAGCCAAAGAGACCGAACTCATGTTG 420

Qy 530 AAGCTTGTGAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGGAGAAACCGAGTTTGTG 589
Db 421 AAGCTTGTGAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGGAGAAACCGAGTTTGTG 480

Qy 590 GCTAGCCAGATGGAGAAATCAATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACTT 649
Db 481 GCTAGCCAGATGGAGAAATCAATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACTT 600

Qy 650 GCTGGAATAATCTCCGACAAATCTTCCGCTGACTCTCCCACTACTTAATTAGCCACCTTAA 709
Db 541 GCTGGAATAATCTCCGACAAATCTTCCGCTGACTCTCCCACTACTTAATTAGCCACCTTAA 600

Qy 710 ATCGCGGTTGAATCAAAATCCAAACATATATATTAATTAAGGAGAAAAAATAAGAT 769
Db 601 ATCGCGGTTGAATCAAAATCCAAACATATATATTAATTAAGGAGAAAAAATAAGAT 660

Qy 770 ATGTAATTAATTCGCTGATAGGCGAGCTTTGTATATCTTAATCTCTCTTTGGCC 829
Db 661 ATGTAATTAATTCGCTGATAGGCGAGCTTTGTATATCTTAATCTCTCTTTGGCC 720

Qy 830 AAGAGACTTTGTGTGATACTTAAAGTAGAGCGAACTAAAGTCAATATCTATCTGTTTAAAG 889
Db 721 AAGAGACTTTGTGTGATACTTAAAGTAGAGCGAACTAAAGTCAATATCTATCTGTTTAAAG 780

Qy 890 ACAAAA 895
Db 781 ACAAAA 786

RESULT 6
US-10-905-520-5
; Sequence 5, Application US/10905520
; Publication No. US20050160499A1
; GENERAL INFORMATION:
; APPLICANT: Richard, AMASINO M.
; TITLE OF INVENTION: VERNALIZATION-RELATED MOLECULES AND METHODS FOR
; INDUCIBLY-CONFERRING EPIGENETIC CHANGES
; FILE REFERENCE: 054030-0076
; CURRENT APPLICATION NUMBER: US/10/905,520
; PRIOR FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US 60/534,835
; PRIOR FILING DATE: 2004-01-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-905-520-5

Query Match 62.7%; Score 591; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.5e-150;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 ATGGGAAGAAAAAATAGAAATCAAGCGAATTCAGAAACAAAGTAGCCGACAAAGTCAC 169
Db 1 ATGGGAAGAAAAAATAGAAATCAAGCGAATTCAGAAACAAAGTAGCCGACAAAGTCAC 60

Qy 170 TTCTCCAAAGCTCGCAAGGCTCTCATCGAAGAACTGTCAGCTTCTGTTCTCTGTGAC 229
Db 61 TTCTCCAAAGCTCGCAAGGCTCTCATCGAAGAACTGTCAGCTTCTGTTCTCTGTGAC 120

Qy 230 GCATCCGTCGCTCTTCTGTCGTCCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 289
Db 121 GCATCCGTCGCTCTTCTGTCGTCCTCCGCTCCGCAAGCTCTACAGCTTCTCTCCGGC 180

Qy 290 GATAACCTGGTCAAGATCTTGAATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC 349
Db 181 GATAACCTGGTCAAGATCTTGAATCGATATGGGAAACAGCATGCTGATGATCTTTAAAGCC 240

Qy 350 TTGGATCATCAGTCAGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTGTG 409
Db 241 TTGGATCATCAGTCAGTCAAAAGCTCTGAACTATGGTTTCACTATGAGCTACTTGAACCTTGTG 300

Qy 410 GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTG 469
Db 301 GATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCAACTG 360

Qy 470 GAGGAAACCTTTGAGACTGCGCTCTCCGTGACTAGAGCCAAAGAGACCGAACTCATGTTG 529
Db 361 GAGGAAACCTTTGAGACTGCGCTCTCCGTGACTAGAGCCAAAGAGACCGAACTCATGTTG 420

Qy 530 AAGCTTGTGAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGGAGAAACCGAGTTTGTG 589
Db 421 AAGCTTGTGAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGGAGAAACCGAGTTTGTG 480

Qy 590 GCTAGCCAGATGGAGAAATCAATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACTT 649
Db 481 GCTAGCCAGATGGAGAAATCAATCATGTGGGAGCAGAGCTGAGATGGAGATGTCACTT 540

Qy 650 GCTGGAATAATCTCCGACAAATCTTCCGCTGACTCTCCCACTACTTAATTAG 700
Db 541 GCTGGAATAATCTCCGACAAATCTTCCGCTGACTCTCCCACTACTTAATTAG 591

RESULT 7
US-10-600-948-9

; Sequence 9, Application US/10600948
; Publication No. US20050091717A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard
; APPLICANT: Schomburg, Fritz
; APPLICANT: Michaels, Scott
; APPLICANT: Sung, Si-Bum
; TITLE OF INVENTION: Alteration of Flowering Time in Plants
; FILE REFERENCE: 960296.96871
; CURRENT APPLICATION NUMBER: US/10/600,948
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/09/513,775
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/121,572
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 60/123,455
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Brassica rapa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(588)
US-10-600-948-9

Query Match 47.6%; Score 448.6; DB 10; Length 867;
Best Local Similarity 84.2%; Pred. No. 2.3e-111;
Matches 543; Conservative 0; Mismatches 94; Indels 8; Gaps 3;

QY 110 ATGGGAAGAAAAAAGCTAGAAATCAAGCGAATTGAGAAACAAAGTAGCCGACAAAGTCACC 169
DB 1 ATGGGAAGAAAAAAGCTAGAAATCAAGCGAATTGAGAAACAAAGTAGCCGACAAAGTCACC 60

QY 170 TTCTCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGAC 229
DB 61 TTCTCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGAC 120

QY 230 GCATCCGTCGCTTCTCTGTCGTCGCTCGGCTCGGCAAGCTCTACAGCTTCTCTCCGGC 289
DB 121 GCATCTGTGGGCTTCTCTGTCGTCGCTCGGCTCGGCAAACTCTACAGCTTCTCTCCGG 180

QY 290 GATAACCTGCTCAAGATCTTGCATGATATGGAACACGATGCTGATGATCTTAAAGCC 349
DB 181 GATAGACTGGAGAGATCTTGCATGATATGGAAGAAACATGCTGATGATCTCAATGCC 240

QY 350 TTGGATCATAGTCAAAAGCTCTGAACTATGGTTCACTATGAGCTACTTGAACCTTGTG 409
DB 241 CTGGATCTTCAAGTCAAAATCTCTGAACTATAGTTTCAACCATGAGCTACTGAACTTGTG 300

QY 410 GATAGCAAGCTTGTGGATCAAAATGCAAAATGTGAGTATCGATGCTTCTTCAACTG 469
DB 301 GAAAGCAAGCTTGTGGAAATCAATTG---ATGATGTAAGCGTGGATTCCTCTCGCTGA 357

QY 470 GAGGAACACTTGGAGCTCCCTCTCCGTCATGAGCCAGAGCAAGCACTCATGTTG 529
DB 358 GAAGATCACCTTGGAGCTCCCTCTCTGTAATAGAGCTCGGAAGCAGAACTAATGTTA 417

QY 530 AAGCTTTGTAAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACAGAGTTTGTG 589
DB 418 AAGCTTTGTAAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACAGAGTTTGTG 477

QY 590 GCTAGCAGATCGAGATCAATCATGTGGAGCGAGAGCTGAGATGAGATGTCACCT 649
DB 478 GCTAGTCAATGAGAGAAATCTTGAAGGAGCGGAGCTGATAATATAGAGATGCA 537

QY 650 GCTGAGCAAACTCTCCGA---CAATCTTCGGTGTACTCTCCCACTACTTAATTTAGCCACT 706
DB 538 TCTGAGCAAACTCTCCGACATCAATCTTCTGTAACTCTCCCGCTGCTTAATTAACCACT 597

QY 707 TAAATCGCGGTTGAAATCAAAATCCAAACATATATATATATGA 751

DB 598 TTACTCGCGGTT--AATCAAAATAAGAAACATATAATCTAAAGA 640

RESULT 8
US-10-600-948-7
; Sequence 7, Application US/10600948
; Publication No. US20050091717A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard
; APPLICANT: Schomburg, Fritz
; APPLICANT: Michaels, Scott
; APPLICANT: Sung, Si-Bum
; TITLE OF INVENTION: Alteration of Flowering Time in Plants
; FILE REFERENCE: 960296.96871
; CURRENT APPLICATION NUMBER: US/10/600,948
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/09/513,775
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/121,572
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 60/123,455
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 863
; TYPE: DNA
; ORGANISM: Brassica rapa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(588)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (839)
; OTHER INFORMATION: unsure
US-10-600-948-7

Query Match 46.6%; Score 439; DB 10; Length 863;
Best Local Similarity 83.3%; Pred. No. 9.8e-109;
Matches 537; Conservative 0; Mismatches 100; Indels 8; Gaps 3;

QY 110 ATGGGAAGAAAAAAGCTAGAAATCAAGCGAATTGAGAAACAAAGTAGCCGACAAAGTCACC 169
DB 1 ATGGGAAGAAAAAAGCTAGAAATCAAGCGAATTGAGAAACAAAGTAGCCGACAAAGTCACC 60

QY 170 TTCTCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGAC 229
DB 61 TCCTCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTCTGTGAC 120

QY 230 GCATCCGTCGCTTCTCTGTCGTCGCTCGGCTCGGCAAGCTCTACAGCTTCTCTCCGGC 289
DB 121 GCATCTGTGGGCTTCTCTGTCGTCGCTCGGCTCGGCAAACTCTACAGCTTCTCTCCGG 180

QY 290 GATAACCTGCTCAAGATCTTGCATGATATGGAACACGATGCTGATGATCTTAAAGCC 349
DB 181 GATAGACTGGAGAGATCTTGCATGATATGGAAGAAACATGCTGATGATCTCAATGCC 240

QY 350 TTGGATCATAGTCAAAAGCTCTGAACTATGGTTCACTATGAGCTACTTGAACCTTGTG 409
DB 241 CTGGATCTTCAAGTCAAAATCTCTGAACTATAGTTTCAACCATGAGCTACTGAACTTGTG 300

QY 410 GATAGCAAGCTTGTGGATCAAAATGCAAAATGTGAGTATCGATGCTTCTTCAACTG 469
DB 301 GAAAGCAAGCTTGTGGAAATCAATTG---ATGATGTAAGCGTGGATTCCTCTCGCTGA 357

QY 470 GAGGAACACTTGGAGCTCCCTCTCCGTCATGAGCCAGAGCAAGCACTCATGTTG 529
DB 358 GAAGATCACCTTGGAGCTCCCTCTCTGTAATAGAGCTCGGAAGCAGAACTAATGTTA 417

QY 530 AAGCTTTGTAAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACAGAGTTTGTG 589
DB 418 AAGCTTTGTAAGATCTTAAAGAAAGGAGAAATGCTGAAAGAGAGAACAGAGTTTGTG 477

Qy 590 GCTAGCCAGATGGAGAAATATCATCTGTTGGAGCAGAGCTGAGATGGAGATGCACCT 649
Db 478 GCTAGTCAGATGGAGAGAAATCTTGAGGAGCGGAAGCTGATTAATATAGAGATGTCA 537
Qy 650 GCTGACAAATCTCCGA---CAATCTTCGGTGACTCTCCCACTACTTAAATTTAGCCACT 706
Db 538 TCTGACAAATCTCCGACATCAATCTTCTGTACTCTCCGCTGCTTAAATTAACCACT 597
Qy 707 TAAATCGCGGTGAAATCAAAATCAAAACATATATAATTAATGA 751
Db 598 TTACTCGCGGT--AATCAAAATAGAAACATATATAATCTAAAGA 640

RESULT 9

US-11-172-740-578
; Sequence 578, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
; APPLICANT: MASCIA, Peter
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
; FILE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; FILE REFERENCE: 2750-1602PUS2
; CURRENT APPLICATION NUMBER: US/11/172,740
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,621
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,800
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 578
; LENGTH: 884
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(884)
; OTHER INFORMATION: Ceres CLONE ID no. 92459
; NAME/KEY: misc.feature
; LOCATION: (1)..(884)
; OTHER INFORMATION: Also known as Ceres CDNA ID no. 23361912
US-11-172-740-578

Query Match 39.6%; Score 373.6; DB 16; Length 884;
Best Local Similarity 73.9%; Pred. No. 7.1e-91;
Matches 517; Conservative 0; Mismatches 174; Indels 9; Gaps 3;
Qy 70 AGGATCAAAATAGGGCAAAAGCCCTCTCGAGA---GAAGCCATGGGAAGAAAAAAT 126
Db 1 AGGATTAATATAGGCA-TAACCTTATCGAGATTTGAAGCCATGGGAAGAAAAAT 59
Qy 127 AGAAATCAAGCAATTCAGAACAAAGTAGCCGAAGTCACTTCTTCCAAAGCTCGCAA 186
Db 60 CGAGATCAAGCAATTCAGAACAAAGTAGCCGAAGTCACTTCTTCCAAAGCTCGCAA 119
Qy 187 CGGTCTCATCGAAGCACTGTCAGCTTCTGTCTCTGTGAGCCATCCGTCGCTCTTCT 246
Db 120 TGGTCTCATCGAAGCACTGTCAGCTTCTGTCTCTGTGAAATCTTCCGTCGCTGTGT 179
Qy 247 CGTCTCTCGCCCTCCGGCAGCTCTACAGCTTCTCTCGGCGATAACCTGGTCAAGAT 306
Db 180 CGTCTATCTCGCTCCGGAAAACTCTATGACTTCTCTCGGTGACGACATTTCCAAGAT 239
Qy 307 CTTGTATCGATAGGGAAAAAGCATGCTGATGATCTTAAAGCCCTTGGATCATCAGTCAAA 366
Db 240 CATTTGCTGTTAATAACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 299
Qy 367 AGCTCTGACTATGGTTTACACTATGAGCTACTTGAACCTTGTGATAGCAAGCTTGTGGG 426

Db 300 AATTGAGAAATATCTTCCACACAAGGAGTTACTAGNAACAGTCCAAAGCAAGCTTTGAAGA 359
Qy 427 ATCAAAATGTCAAAATATGTAGTATCGATGCTCTTGTTCAACTGGAGGAACACCTTTGAGAC 486
Db 360 ACCAAATGTGATTAATGTAGTGTAGATCTCTTAATTTCTCTGGAGGAACAACTTGAGAC 419
Qy 487 TGCCCTCTCCGTGACTAGAGCCAAAGAGACGAACACTCATGTTGAAGCTTTGTTGAGAAATCT 546
Db 420 TGCTCTGTCGTAAGTAGAGCTAGGAAGGCGAGAACTGATGATGAGTATATCGAGTCCCT 479
Qy 547 TAAAGAAAGGAGAAATGCTGAAAGAGAGAACCAAGTTTGGCTAGCCAGATGGAGAA 606
Db 480 TAAAGAAAGGAGAAATTTGCTGAGAGAGAGAACCAAGTTTGGCTAGCCAGATGGAGAA 539
Qy 607 TAATCATCATGTGGAGCAGAAAGCTGAGATGGAGATGTCACCTGCTGGACAAAATCTCCGA 666
Db 540 GAATACGTTGCTGCAACAGATGATGAGAGAGGAGATGTTTCCGGAAGTAGCTCGGCNA 599
Qy 667 CAATCTTCGGTGACTCTCCCACTATCTTAATTTAGCCACCTT-----AAATCGGCGTTGA 721
Db 600 CAAATACCGGAGACTCTCCGCTGCTCAATTTAGCCACCATCATCAACGGCTGAGTTTTC 659
Qy 722 AATCAAAATCCAAACATATATAATTTATGAGAAAAAAA 761
Db 660 ACCTTAAATCCAAAGCCCTGATTTCATAATTAAGAGAAATANA 699

RESULT 10

US-10-225-066A-1087
; Sequence 1087, Application US/10225066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI0036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1087
; LENGTH: 883
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-1087

Query Match 39.5%; Score 372.6; DB 7; Length 883;
Best Local Similarity 73.8%; Pred. No. 1.3e-90;
Matches 489; Conservative 0; Mismatches 169; Indels 5; Gaps 1;
Qy 104 GAAGCCATGGGAAGAAAAAATAGAAATCAAGCGAATTGAGAAACAAAGTAGCCGACAA 163


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Db 25 GAAGCCATGGGAAGAGAAATAATCGAGATCAAGCGAATCGAGAAACAAAGACGTCGACAA 84
Qy 164 GTACACTTCTCCAAACCTCCCAACGCTCTCATCGAGAAAGCTGGTCAAGCTTTCTGTCTC 223
Db 85 GTCACTTCTCCAAACACGCAATGGTCTCATCGACAAAGCTCGACAACTTTTCAATCTC 144
Qy 224 TGTGACGCATCCGTCGCTCTTCTCGTCTCCGCTCTCCGCTCCGCAAGCTCTACAGCTTCTCC 283
Db 145 TGTGAATCTCTCGTCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 204
Qy 284 TCCGGCGATCAACCTGGTCAAGATCTTGTGATCGATATGGGAAAACAGCATGCTGATGATCTT 343
Db 205 TCCGGTCAAGCAATTTTCAAGATCATGATCGTATGATGATGATGATGATGATGATGATG 264
Qy 344 AAAGCCTTGGATCATCATGATCAAGCTCTCAATGATGATGATGATGATGATGATGATGAT 403
Db 265 AGAGCCTTAGATCTTGAAGAAAATAATTCAGAAATTTATCTTCCACACAAAGGAGTACTAG 324
Qy 404 CTGTGTGATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGATGATGATGATGATGATG 463
Db 325 ACAGTCCAAAGCAAGCTTGAAGAACCAATGTGATGATGATGATGATGATGATGATGATG 384
Qy 464 CAAGTGGAGAAACCTTGGAGACTGCCCTCTCCGCTAGAGCCCAAGAGACCGAACTC 523
Db 385 TCTCTGGAGGAACAACCTTGGAGACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
Qy 524 ATGTTGAGCTTGTGAGAAATCTTAAAGAAAAGGAGAAAATCTGAAAAGAGAACCCAG 583
Db 445 ATGATGGAGTATATCGAGTCCCTTAAAGAAAAGGAGAAATTCCTGAGAGAGAGAACCC 504
Qy 584 GTTTTGGCTAGCCAGATGGAGAAATATCATCATGTTGGGAGAGAGAGCTGAGATGGAGATG 643
Db 505 GTTCTGGCTAGCCAGATGGAGAAATATCATCATGTTGGGAGAGAGAGCTGAGATGGAGATG 564
Qy 644 TCACCTGCTGGAGAAATCTCCGACAACTCTCCGCTGACTCTCCCACTACTCTTAATAGCCA 703
Db 565 TTTCCGGGAAGTAGCTCCGGCAACAAATAACCGGAGACTCTCCGCTGCTCAATAGCCA 624
Qy 704 CCTT-----AAATCGCGGTGGAATCAAAATCAAAATCAAAATCAAAATCAAAATCA 758
Db 625 CCATCATCAACGGCTGAGTTTTTCACTTAAACTCAAAAGCCTGATTCATAATTAAGAAAT 684
Qy 759 AAA 761
Db 685 AAA 687
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RESULT 11

US-10-374-780A-15

; Sequence 15, Application US/10374780A

; Publication No. US20040019927A1

; GENERAL INFORMATION:

; APPLICANT: Sherman, Bradley K

; APPLICANT: Riechmann, Jose Luis

; APPLICANT: Jiang, Cai-Zhong

; APPLICANT: Heard, Jacqueline E

; APPLICANT: Haake, Volker

; APPLICANT: Creelman, Robert A

; APPLICANT: Ratcliffe, Oliver

; APPLICANT: Adam, Luc J

; APPLICANT: Reuber, T. Lynne

; APPLICANT: Keddle, James

; APPLICANT: Brown, Pierre E

; APPLICANT: Filgrim, Marsha L

; APPLICANT: Dubell III, Arnold T

; APPLICANT: Pineda, Omaira

; APPLICANT: Yu, Guo-Liang

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

; FILE REFERENCE: MBI-0047 CIP

; CURRENT APPLICATION NUMBER: US/10/374,780A

; CURRENT FILING DATE: 2003-02-25

; PRIOR APPLICATION NUMBER: 09/837,944

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; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 883
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G157
; US-10-374-780A-15
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Query Match 39.5%; Score 372.6; DB 8; Length 883;

Best Local Similarity 73.8%; Pred. No. 1.3e-90;

Matches 489; Conservative 0; Mismatches 169; Indels 5; Gaps 1;

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Qy 104 GAAGCCATGGGAAGAGAAATAATCGAGATCAAGCGAATCGAGAAACAAAGACGTCGACAA 163
Db 25 GAAGCCATGGGAAGAGAGAAATAATCGAGATCAAGCGAATCGAGAAACAAAGACGTCGACAA 84
Qy 164 GTACACTTCTCCAAACCTCCCAACGCTCTCATCGAGAAAGCTGGTCAAGCTTTCTGTCTC 223
Db 85 GTCACTTCTCCAAACACGCAATGGTCTCATCGACAAAGCTCGACAACTTTTCAATCTC 144
Qy 224 TGTGACGCATCCGTCGCTCTTCTCGTCTCCGCTCTCCGCTCCGCAAGCTCTACAGCTTCTCC 283
Db 145 TGTGAATCTCTCGTCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 204
Qy 284 TCCGGCGATCAACCTGGTCAAGATCTTGTGATCGATATGGGAAAACAGCATGCTGATGATCTT 343
Db 205 TCCGGTCAAGCAATTTTCAAGATCATGATCGTATGATGATGATGATGATGATGATGATG 264
Qy 344 AAAGCCTTGGATCATCATGATCAAGCTCTCAATGATGATGATGATGATGATGATGATGAT 403
Db 265 AGAGCCTTAGATCTTGAAGAAAATAATTCAGAAATTTATCTTCCACACAAAGGAGTACTAG 324
Qy 404 CTGTGTGATAGCAAGCTTGTGGGATCAAAATGTCAAAATGTGATGATGATGATGATGATGATG 463
Db 325 ACAGTCCAAAGCAAGCTTGAAGAACCAATGTGATGATGATGATGATGATGATGATGATG 384
Qy 464 CAAGTGGAGAAACCTTGGAGACTGCCCTCTCCGCTAGAGCCCAAGAGACCGAACTC 523
Db 385 TCTCTGGAGGAACAACCTTGGAGACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
Qy 524 ATGTTGAGCTTGTGAGAAATCTTAAAGAAAAGGAGAAAATCTGAAAAGAGAACCCAG 583
Db 445 ATGATGGAGTATATCGAGTCCCTTAAAGAAAAGGAGAAATTCCTGAGAGAGAGAACCC 504
Qy 584 GTTTTGGCTAGCCAGATGGAGAAATATCATCATGTTGGGAGAGAGAGCTGAGATGGAGATG 643
Db 505 GTTCTGGCTAGCCAGATGGAGAAATATCATCATGTTGGGAGAGAGAGCTGAGATGGAGATG 564
Qy 644 TCACCTGCTGGAGAAATCTCCGACAACTCTCCGCTGACTCTCCCACTACTCTTAATAGCCA 703
Db 565 TTTCCGGGAAGTAGCTCCGGCAACAAATAACCGGAGACTCTCCGCTGCTCAATAGCCA 624
Qy 704 CCTT-----AAATCGCGGTGGAATCAAAATCAAAATCAAAATCAAAATCAAAATCA 758
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/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: 09/394,519
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: 09/489,376
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: 09/506,720
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 09/533,030
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,392
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,029
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/532,591
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,648
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/713,994
/ PRIOR FILING DATE: 2000-11-16
/ PRIOR APPLICATION NUMBER: 09/819,142
/ PRIOR FILING DATE: 2001-03-27
/ Remaining prior application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2011
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1733
/ LENGTH: 883
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-10-412-699B-1733

Query Match      39.5%; Score 372.6; DB 8; Length 883;
Best Local Similarity 73.8%; Pred. No. 1.3e-90;
Matches 489; Conservative 0; Mismatches 169; Indels 5; Gaps 1;

QY 104 GAAGCCATGGGAGAAAAAAGTAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAA 163
Db 25 GAAGCCATGGGAGAAAAAATCGAGATCAAGCGAATCGAGAACAAAAGTAGCGACAA 84

QY 164 GTCACTTCTCCAAACGTCGCAAGCTCTCATCGAAGAGCTCGTCAGCTTTCTGTCTC 223
Db 85 GTCACTTCTCCAAACGAGCAATGGTCTCATCGAAGAGCTCGACAACTTTGATTTCTC 144

QY 224 TGTGACGCATCGTCTGCTCTTCTCGTCTCTCCGCTCGGCAAGCTCTACAGCTTCTCC 283
Db 145 TGTGAATCCTCGTCTGCTTGTGTCGTCTCGTCTCGGAAAACTCTATGACTTCTCC 204

QY 284 TCCGCGGATAAATCCTGGTCAAGATCCTTGATCGATATGGAAACAGCATGCTGATGATCTT 343
Db 205 TCCGCTGACGACATTTCCAGATCATTTGATGATGATGATGATGATGATGATGATGATGAT 264

QY 344 AAAGCTTTGGATCATCATGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 403
Db 265 AGAGCTTTAGATCTTTGAAGAAAAAATTCAGAAATATCTTCCACACAGGAGTTACTAGAA 324

QY 404 CTTGTGGATAGCAAGCTTTGTGGGATCAAAATGTCAAAATATGTGAGTATCGATGCTTTGTT 463
Db 325 ACAGTCCAAAGCAAGCTTCAAGAACCAATATGATATGATATGATATGATATGATATGATAT 384

QY 464 CAAGTGGAGAACACCTTGAGACTGCCCTCTCGTGACTAGAGCCCAAGAACCGAATCTC 523
Db 385 TCTCTGGAGAACCACTTGAGACTGCTCTGTCCGTAAGTAGAGCTAGGAGGAGCAAGCTG 444

QY 524 ATGTTGAAGCTTTGAGAAATCTTAAAGAAAGGAGAAATGCTGAAGAACGAGAACCAAG 583
Db 445 ATGATGGAGTATATCGAGTCCCTTAAAGAAAGGAGAAATGCTGAGAGAGAGAACCAAG 504

QY 584 GTTTTGGCTAGCCAGATGGAGAAATATCATATGTGGGAGCAGAAAGCTGAGATGGAGATG 643
Db 505 GTTCTGGCTAGCCAGATGGGAAAGATACTGTTGCTGGCAACAGATGATGAGAGAGGATG 564

QY 644 TCACCTGTGGACAAATCTCCGACATCTTCGGTGACTCTCCGACTACTTAAATTAGCCA 703
Db 565 TTTCCGGGAGTAGCTCCGGCAACAAATACCGGAGACTCTCCGCTGCTCAATTAGCCA 624

QY 704 CCTT-----AAATCGCGGTGGAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAAT 758
Db 625 CATCATCAACGGCTGAGTTTTTCACTTAACTCAAGGCTGATTTATTAATTAAGAGAT 684

QY 759 AAA 761
Db 685 AAA 687

RESULT 14
US-10-225-066A-1087
/ Sequence 1087, Application US/10225066A
/ Publication No. US20050160493A9
/ GENERAL INFORMATION:
/ APPLICANT: Mendel Biotechnology, Inc.
/ APPLICANT: RATCLIFFE, Oliver
/ APPLICANT: RIECHMANN, Jose Luis
/ APPLICANT: ADAM, Luc J
/ APPLICANT: DUBELL, Arnold T
/ APPLICANT: HEARD, Jacqueline E
/ APPLICANT: FILGRIM, Marsha L
/ APPLICANT: JIANG, Cai-Zhong
/ APPLICANT: REUBER, T. Lynne
/ APPLICANT: CREELMAN, Robert A
/ APPLICANT: PINEDA, Omaira
/ APPLICANT: YU, Guo-Liang
/ APPLICANT: BROWN, Pierre E
/ TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
/ FILE REFERENCE: MB10036-2 US
/ CURRENT APPLICATION NUMBER: US/10/225,066A
/ CURRENT FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: 09/837,444
/ PRIOR FILING DATE: 2001-04-18
/ PRIOR APPLICATION NUMBER: 60/310,847
/ PRIOR FILING DATE: 2001-08-09
/ PRIOR APPLICATION NUMBER: 60/336,049
/ PRIOR FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: 60/338,692
/ PRIOR FILING DATE: 2001-12-11
/ PRIOR APPLICATION NUMBER: 10/171,468
/ PRIOR FILING DATE: 2002-06-14
/ NUMBER OF SEQ ID NOS: 1122
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1087
/ LENGTH: 883
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-10-225-066A-1087

Query Match      39.5%; Score 372.6; DB 10; Length 883;
Best Local Similarity 73.8%; Pred. No. 1.3e-90;
Matches 489; Conservative 0; Mismatches 169; Indels 5; Gaps 1;

QY 104 GAAGCCATGGGAGAAAAAAGTAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAA 163
Db 25 GAAGCCATGGGAGAAAAAATCGAGATCAAGCGAATCGAGAACAAAAGTAGCGACAA 84

QY 164 GTCACTTCTCCAAACGTCGCAAGCTCTCATCGAAGAGCTCGTCAGCTTTCTGTCTC 223
Db 85 GTCACTTCTCCAAACGAGCAATGGTCTCATCGAAGAGCTCGACAACTTTGATTTCTC 144

QY 224 TGTGACGCATCGTCTGCTCTTCTCGTCTCTCCGCTCGGCAAGCTCTACAGCTTCTCC 283
Db 145 TGTGAATCCTCGTCTGCTTGTGTCGTCTCGTCTCGGAAAACTCTATGACTTCTCC 204

QY 284 TCCGCGGATAAATCCTGGTCAAGATCCTTGATCGATATGGAAACAGCATGCTGATGATCTT 343
Db 205 TCCGCTGACGACATTTCCAGATCATTTGATGATGATGATGATGATGATGATGATGATGAT 264

QY 344 AAAGCTTTGGATCATCATGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 403
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QY 404 CTTGTGATAGCAAGCTTGGGATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGT 463
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QY 325 ACGATCCAAAGCAAGCTTGAAGAACCAAAATGTGATAATGTAAAGTGTAGATTCTCTAAT 384
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QY 464 CAACTGGAGGAACACCTTGGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAACCGAATC 523
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QY 395 TCTCTGGAGGAACAATCTGGAGACTGCTCTGCTCGTAAGTAGAGCTAGGAGGCAGACTG 444
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QY 524 ATGTTGAAGCTTGTGAGAACTTAAAGAAAGGAGAAATCTGAAAGAGAGAACCCAG 583
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QY 505 GTTCTGGCTAGCAGATGGAGAAATAGCTTGTGGCAACAGATGATGAGAGAGGAATG 564
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QY 704 CCTT-----AAATCGCGGTGAAATCAAAATCCHAAAACATATATAATTTAGAGAAAA 758
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QY 625 CCATCATCAACGGCTGAGTTTTCACCTTAAACTCAAGCCTGATTTCATAATTAAGAGAT 684
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QY 685 AAA 687

RESULT 15

US-10-225-066A-1055
; Sequence 1055, Application US/10225066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Mareha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MB10036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-1055

Query Match 38.6%; Score 363.8; DB 7; Length 1059;
Best Local Similarity 73.9%; Pred. No. 3.7e-88;
Matches 475; Conservative 0; Mismatches 167; Indels 1; Gaps 1;

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QY 176 TTAGATCAAAATTAGGGCAAAAGCCTTATCGGAGAAAGAGCCATGGGAAGAAAAAGT 235
Db |||||
QY 127 AGAATCAAGCGAATTTGAGAACAAAGTAGCGGCAAGTCACTTCTCCAAAGCTGCGAA 186
Db |||||
QY 236 CGAGATCAAGCGAATTCGAGAACAAAGCAGTCGACAGTCACTTTCTCCAAACGACGCA 295
Db |||||
QY 187 CGGTCTCATCGAGAAAGCTCGTCAAGCTTTCTGTGTCTCTGTGACGATCCGTGCGCTTCT 246
Db |||||
QY 296 AGGTCTCATCGAAGAGCTCGACAACTTTCAATTTCTGTGAACTTCCATCGCTGTGT 355
Db |||||
QY 247 CGTGTCTCCGCTCCCGCAAGCTCTACAGCTTCTCTCCGCGGATAACCTGGTCAAGAT 306
Db |||||
QY 356 CGCGTCTCCGCTCCGGAAGCTCTACGACTCTGCGCTCCGTTGACAAACATGTCAAAGAT 415
Db |||||
QY 307 CTTGTGATGATGGGAACAGCATGCTGATGATCTTAAAGCCTTGGATCATCATGCAAA 366
Db |||||
QY 416 CATTTGATGTTTATGAATAATCATCATGCTGATGAATCTTAAAGCCTTTAGATCTTGCAGNAAA 475
Db |||||
QY 367 AGCTCTGAATATGTTTCACTATGAGCTACTTGAACCTTGTGATAGCAAGCTTGTGGG 426
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QY 476 AATTGCGAATTTATCTTCCACACAGGAGTTACTAGAAATAGTCCAAAGCAAGCTTGAAGA 535
Db |||||
QY 427 ATCAAAATGTCAAAATGTGAGTATCGATGCTCTTGTTCACCTGGAGGAACACCTTGAAC 486
Db |||||
QY 536 ATCAAAATGTGATTAATGTAAAGTGTAGATTTCTCTAATATCTATGAGGAAACAGCTCGAGAC 595
Db |||||
QY 487 TGCCTCTCCGTGACTAGGCCAAGAGACCGAATCTCATGTTGAAGCTTGTGAGAACT 546
Db |||||
QY 596 TGCTCTGTGATTAATGAGGCTTAAGAGACAGAACTAATGATGAGGATATGAAAGTCACT 655
Db |||||
QY 547 TAAAGAAAGGAGAAATTCGTAAGAGAGAACAGGTTTGTGCTAGCCAGATGGAGAA 606
Db |||||
QY 656 TCAAGAAAGGAGAGAGTTGCTGATGAGAGAACAGATTTCTGGCTAGCCAGGTGGGAA 715
Db |||||
QY 607 TAATCATCATGTGGAGCAGAGCTGAGATGGAGATGTCACTCTGTGGAACAAATCTCGA 666
Db |||||
QY 716 GAAGACGTTTCTGCTTATAGAAAGGTGACAGAGGAATGTACGGGAAATGCTCCGGCA 775
Db |||||
QY 667 CAATCTTCGGTGACTCTCCCACTACTTAATTAGCCACCTTAA 709
Db |||||
QY 776 CAAAGTACCGGAGACTCTTTGCTGCTCAAGTAATCACCATCA 818
Db |||||

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Perfect score: 943
Sequence: 1 CGAGAAAAGGAAAAA.....tGAGAAAAA 943

Scoring table: IDENTITY_NUC
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Searched: 224314 seqs. 35277956 residues

Total number of hits satisfying chosen parameters: 448628

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Maximum DB seq length: 2
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /EMC Celerra SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq.*

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SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	7.1	67	549	7	US-11-217-529-4894	Sequence 4894, Ap	
2	7.0	65.8	858	7	US-11-217-523-77960	Sequence 77960, Ap	
3	6.8	63.8	846	7	US-11-217-529-1966	Sequence 1966, Ap	
4	5.9	56	1968	7	US-11-217-529-2608	Sequence 2608, Ap	
5	5.8	54.8	4077	6	US-10-505-928-134	Sequence 134, App	
6	5.8	54.4	534	7	US-11-217-529-77959	Sequence 77959, A	
7	5.3	49.6	804	7	US-11-217-529-82725	Sequence 82725, A	
8	4.9	46.4	1362	7	US-11-217-529-2782	Sequence 2782, Ap	
9	4.8	44.8	1359	7	US-11-217-529-75588	Sequence 75588, A	
10	3.7	39	1503	7	US-11-217-529-1897	Sequence 1897, Ap	
C 11	3.6	33.6	475	6	US-10-488-613-1723	Sequence 1723, Ap	
12	3.6	33.6	4464	7	US-11-217-529-76543	Sequence 76543, A	
13	3.5	33.4	2700	7	US-11-217-529-77867	Sequence 77867, A	
14	3.5	33.2	1765	1	US-09-949-925-55	Sequence 55, Appl	
15	3.5	33	641	6	US-10-488-613-1577	Sequence 1577, Ap	
16	3.5	32.8	786	7	US-11-217-529-81354	Sequence 81354, A	
17	3.5	32.8	1556	6	US-10-505-928-322	Sequence 322, App	
18	3.5	32.6	918	7	US-11-217-529-1084	Sequence 1084, Ap	
19	3.4	32.4	1551	7	US-11-217-529-78695	Sequence 78695, A	
20	3.4	31.8	592	6	US-10-488-619-1012	Sequence 1012, Ap	
21	3.4	31.6	34	3	US-10-511-937-414	Sequence 414, App	
C 22	3.4	31.6	394191	6	US-10-506-549-3	Sequence 3, Appli	
C 23	3.3	31.4	228	7	US-11-217-529-166541	Sequence 166541, A	
24	3.3	31.4	677	6	US-10-488-619-1302	Sequence 1302, Ap	
25	3.3	31.4	855	7	US-11-217-529-5202	Sequence 5202, Ap	

ALIGNMENTS

RESULT 1

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US-11-217-529-4894
; Sequence 4894, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4894
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4894

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RESULT 2

US-11-217-529-77960
; Sequence 77960, Application US/11217529
; Publication No. US20060039612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED

APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHIISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 77960
LENGTH: 858
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-77960

Query Match 7.0%; Score 65.8; DB 7; Length 858;
Best Local Similarity 60.2%; Pred. No. 4.5e-09;
Matches 109; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 105 AGCCATGGAGAGAAAAAAGTGAATCAAGCGAATTCAGAACAAAAAGTAGCCGCAAG 164
DB 41 AACAGAGAGAGAGAGAGAGATAGAAATTAAGTTTCATCGAGAAATAAAACAAGCGCCATG 100
QY 165 TCACCTTCTCCAAAGCTCGCAAGGCTCATCGAGAAAGCTCGTCAAGTTTCTGTTCTCT 224
DB 101 TGACATTTCCAAAGAGACGCGGTATCAAGAAAGCGTTTGAGCTTTCTGTTCTAA 160
QY 225 GTGACGATCCGTCGCTCTTCTCGTCTCGCCCTCGGCAAGCTCTACAGCTTCTCTCT 284
DB 161 CGGGAGCCAGGTCCTGTTGCTAGTCTGTTTCAGAAACAGGTTTGGTATATACCTTCAGCA 220
QY 285 C 285
DB 221 C 221

RESULT 3
US-11-217-529-1966
; Sequence 1966, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1966
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1966

Query Match 6.8%; Score 63.8; DB 7; Length 846;
Best Local Similarity 60.8%; Pred. No. 1.6e-08;
Matches 104; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 110 ATGGGAGAGAGAGAGAGATAGAAATCAAGCGAATTCAGAACAAAAAGTAGCCGCAAGTCACC 169
DB 46 AAGGAGAGAGAGAGAGATAGAAATCAAGTTTATGAGAAATAAAACAAGCGCCATGTGACT 105

QY 170 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGAC 229
DB 106 TTTTCCAGAGAGAGAGAGAGATCATGAAGAGGCGTTCGAGCTGTCTGTCTGACAGGT 165
QY 230 GCATCCGTCGCTTCTCTCGTCTCGCTCCGCTCCGGCAAGCTCTACAGCTTCTC 280
DB 166 AGCAGGTCGCTGTGCTGTTGCTCTCAGAGACGGGTTTGGTGTACACTTTC 216

RESULT 4
US-11-217-529-2608
; Sequence 2608, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2608
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2608

Query Match 5.9%; Score 56; DB 7; Length 1968;
Best Local Similarity 56.5%; Pred. No. 3.1e-06;
Matches 104; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 110 ATGGGAGAGAGAGAGAGATCAAGCGAATTCAGAACAAAAAGTAGCCGCAAGTCACC 169
DB 1 ATGGGTAGACGTAAATTTGAGATCCAAAGGATTTCTGATGATAGAAACAGGCTGTGACC 60
QY 170 TTCTCCAAACGTCGCAACGGTCTCATCGAGAAAGCTCGTCAGCTTTCTGTTCTCTGTGAC 229
DB 61 TTCATAAGAGCTTAAGCGGGCTTTTCAAAAAGGCCATGAATCTCCGTTCTTTGCCAA 120
QY 230 GCATCCGTCGCTTCTCTCGTCTCGCTCCGCTCCGGCAAGCTCTACAGCTTCTCCTCCGCG 289
DB 121 GTAGATATAGCGGTTATCATACTGGGCTCCAACATACTTTCTATGAATTTTCTCCTCGTG 180
QY 290 GATA 293
DB 181 GATA 184

RESULT 5
US-10-505-928-134
; Sequence 134, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 134
; LENGTH: 4077
; TYPE: DNA
; ORGANISM: Homo sapiens


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US-10-505-928-134
Query Match          5.8%; Score 54.8; DB 6; Length 4077;
Best Local Similarity 55.9%; Pred. No. 9.5e-06;
Matches 104; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 108 CCATGGGAAGAAAAAATAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAAAGTCA 167
Db 400 CTATGGGAGAAAAAGAAATTAGATTACAGAGATTATGGATGACGTAACAGACAGGTGA 459
Qy 168 CTTTCTCCAAAGTCGCAACGGTCTCATCGAAGAGCTCGTCAGCTTTCTGTCTCTGTG 227
Db 460 CATTACAAAGAGAAATTTGGTTGATGAAGAGGCTTATGAGCTGAGCGTGTCTGTG 519
Qy 228 ACGCATCGCTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCG 287
Db 520 ACTGTGAGATTGCGCTGATCATCTTCAACAGCACCAACAGCTGTTCCAGTATGCCAGCA 579
Qy 288 GCGATA 293
Db 580 CCGACA 585

RESULT 6
US-11-217-529-77959
; Sequence 77959, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77959
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77959

Query Match          5.8%; Score 54.4; DB 7; Length 534;
Best Local Similarity 59.9%; Pred. No. 4.3e-06;
Matches 91; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 131 ATCAAGCGAATTGAGAACAAAAGTAGCCGACAAAGTCAACCTTCTCCAAACGTCGCAACGGT 190
Db 253 ATCAGGTACATCGAGATAATAGCCGAGACATGTACCTTCTCGAAGAGCGGACGGG 312
Qy 191 CTCAATCGAAGAGCTCGTCAGCTTTCTGTGTGACGATCCGTCGCTCTTCTCTGTC 250
Db 313 ATCATGAAAAAGCATATGAGCTCTCGTCTTACCGGGGCAATATCTGCTCTTAATT 372
Qy 251 GTCTCCGCTCCGCGAAGCTTCTACAGCTTCTC 282
Db 373 CTGGCAAACTCTGGCCTGGTCTACACTTTTCA 404

RESULT 7
US-11-217-529-82725
; Sequence 82725, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
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; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82725
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82725

Query Match          5.3%; Score 49.6; DB 7; Length 804;
Best Local Similarity 54.3%; Pred. No. 0.0001;
Matches 100; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 110 ATGGGAAGAAAAAATAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAAAGTCA 169
Db 1 ATGGGTAGACGGAAGATTGAAATCCAGAGGATTTCTGTATGACAGAAATAGGGCTGTCA 60
Qy 170 TTCTCCAAACGTCGCAACGGTCTCATCGAAGAGCTCGTCAGCTTTCTGTCTCTGTGAC 229
Db 61 TTTATAAAGCGTAAGCTGGCCCTTTTAAAGAGGCCCATGAACATATCCGTTCTTTGTCAA 120
Qy 230 GCATCCGTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGGC 289
Db 121 GTAGACATAGCCGTCAATTATCTGCGGTCCAATAACACGTTCTATGAGTTTTCTCTGTG 180
Qy 290 GATA 293
Db 181 GATA 184

RESULT 8
US-11-217-529-2782
; Sequence 2782, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2782
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2782

Query Match          4.9%; Score 46.4; DB 7; Length 1362;
Best Local Similarity 53.3%; Pred. No. 0.001;
Matches 98; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 110 ATGGGAAGAAAAAATAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAAAGTCA 169
Db 1 ATGGGTAGAAGAAAGATTGAGATTGAGCTTATCAAGCGCATAGAAATCGTACGGTAACT 60
Qy 170 TTCTCCAAACGTCGCAACGGTCTCATCGAAGAGCTCGTCAGCTTTCTGTCTCTGTGAC 229
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Ds 61 TTCTATAAAGCAAGAGGACTTTTCAGAAAAGCTCATGAACCTGTCGGTACTATGCGCAA 120
Qy 230 GCATCCGTCGCTCTCTCGTGTCTCGGCTCCGCGCAAGCTCTACAGCTTCTCTCCGGC 289
Ds 121 GTGATATTGCTGTCTATTATATTGGATCATTAATAATACCTTTTATGAATACTCTTCTGTC 180
Qy 290 GATA 293
Ds 181 GATA 184

RESULT 9

US-11-217-529-75588
; Sequence 75588, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2005-09-02
; NUMBER OF SEQ ID NOS: 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75588
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75588

Query Match 4.8%; Score 44.8; DB 7; Length 1359;
Best Local Similarity 52.7%; Pred. No. 0.0027;
Matches 97; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
Qy 110 ATGGGAGAAAAAATAGAAATCAAGCGAATTGAGAACAAAAGTAGCCGACAAAGTCACC 169
Ds 1 ATGGGTAGAGAAAAAATGAAATGGAACCTATCAAGATGATAGAAATCGTACAGTTACT 60
Qy 170 TTCTCAAAAGCTGCCAAGCTCTCATCGAGAAAGCTCTCAGCTTTCTGTCTCTGTGAC 229
Ds 61 TTCTAAAGCAAGAGAGAGCTTTTAAAGGCTCATGAATGTGACGACTTTTGGCCAA 120
Qy 230 GCATCCGTCGCTCTCTCGTGTCTCGGCTCCGCGCAAGCTCTACAGCTTCTCTCCGGC 289
Ds 121 GTAGACATTGCTGTCTATTATTTAGGATCCAATAATACATTCTACGATATCTTCTGTT 180
Qy 290 GATA 293
Ds 181 GATA 184

RESULT 10

US-11-217-529-1697
; Sequence 1697, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1697
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1697

Query Match 3.3%; Score 37.2; DB 7; Length 1503;
Best Local Similarity 50.6%; Pred. No. 0.32;
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
Qy 458 CTTGTTCAACTGGAGGAAACACCTTGGAGACTGCCCTCTCCGTGACTAGAGCCAAAGAGACC 517
Ds 922 CTTATTTGGCTTGAAGAATAGGTTACATGGACTTTGATGAACAACGCAAAAAGACG 981
Qy 518 GAACTCATGTTGAAGCTTTGTTGAGAAATCTTAAAGAAAAGGAGAAAATGCTGAAAGAGAG 577
Ds 982 ACGCAAGAGGAGAGAAATCGGATCGAATGAAGATGACAAAAATATTGAACACAGAAACATGAC 1041
Qy 578 AACCAGTTTTGGCTAGCCAGATGGAGAAATATCATCATGTTGGAGCAGAGAGCTGAGA 635
Ds 1042 CATGAGGTTTGTGATGCGCAAGATTGATGGTACCGAAAAGTGTTCATGACAAATGATGATA 1099

RESULT 11

US-10-488-619-1723/c
; Sequence 1723, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P. C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1723
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1723

Query Match 3.6%; Score 33.6; DB 6; Length 475;
Best Local Similarity 51.3%; Pred. No. 1.6;
Matches 78; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
Qy 490 CCTCTCCGTGACTAGAGCCAAAGACCGAACTCATGTTGAAGCTTGTGAGAACTTAA 549
Ds 163 CTTCTCCGAGCTGGCTGAGGACAAAGAAACGGGAGAGGAGATCAGTGATGATGAGGC 104
Qy 550 AGAAAAGGAGAAAATGCTGAAAAGAGAGAACAGAGTTTGGCTAGCCAGATGGAGAAATA 609
Ds 103 AGAGGAGAGAAAGGTGAGAAAGAGGAGAAATAGGAGGATGAGGAGAGCCTAAGAT 44
Qy 610 TCATCATGTTGGAGCAGAGCTGAGATGGAGA 641
Ds 43 TGAAGATGTGGATCCGATGAGGAAAGATGACA 12

RESULT 12

US-11-217-529-76543
; Sequence 76543, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

```

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76543
; LENGTH: 4464
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76543

Query Match          3.6%; Score 33.6; DB 7; Length 4464;
Best Local Similarity 52.9%; Pred. No. 5.3;
Matches 72; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 713 GCGCGTTGAAATCAAAATCCAAACATATATAATTAAGAGAAAAAATAAGATATG 772
DB 3249 GACCTTTGCGACCAAACTCTGAATCTCTAAGGTGATGAGAAAAAACAATCTTA 3308
QY 773 TAATTAATTCGCTGATAGGCGAGCGTTTGTATATCTTAATCTCTCTTTGGCCAAG 832
DB 3309 TTTGACTTCAACAGCAATACTATCAGGAACCTGTTGAAATTAAGCTGCGCTGGAGATAT 3368
QY 833 AGACTTTGTGTGAT 848
DB 3369 CGACAATGGGTATTAT 3384

RESULT 13
US-11-217-529-77867
; Sequence 77867, Application US/11217529
; Publication No. US2006099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIOHRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77867
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77867

Query Match          3.5%; Score 33.4; DB 7; Length 2700;
Best Local Similarity 49.7%; Pred. No. 4.6;
Matches 85; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 499 GACTAGAGCCAGAGACCGAATCACTGTTTGAAGCTTTGTGAGATCTTAAAGAAAGGA 558
DB 1350 GGCTTAAGATATGATCAATCAACATGGTATGACAAATGACGCTGAAACCGAGAGAAATGGA 1409
QY 559 GAAATGCTCAAGAGAACAGACAGGTTTGGCTAGCCAGATGGAGAAATAATCATCATGT 618
DB 1410 AGAGATGCTAAGACAGGTGACGTTTAAAGGCAAAATGTTGGATGAAATCTGATGA 1469
QY 619 GGAGCAGAGAGCTGAGATGGAGATGTCACCTGCTGGACAATCTCCGACAA 669
DB 1470 TGAAGAGGATGGTGGTGTGCAACATTAAGTGATGTTGAAATGAGGAGAA 1520
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RESULT 14

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US-09-949-925-55
; Sequence 55, Application US/09949925
; Publication No. US2006099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 1765
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-925-55
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Query Match          3.5%; Score 33.2; DB 1; Length 1765;
Best Local Similarity 48.9%; Pred. No. 4.2;
Matches 89; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
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QY 261 CCGCGAAGCTCTACAGCTTCTCTCCGCGCATTAACCTGGTCAAGATCCTTGATCGATATG 320
DB 241 CAGCCAAAGTTTAATTAATCTCTGCTGACGGGACATGCTGTTTCTAATGTATGGGATGG 300
QY 321 GGAACACAGCATGCTGATGATCTTAAAGCCTTGGATCATCATCAAAAGCTCTGAACATG 380
DB 301 TGATAGAGAGTCTCAGGATGAACCTTCTTGATATACATGAACACAGCAGTAGGATT 360
QY 381 GTTCACATATGAGCTACTTGAACCTTGTGGATAGCAAGCTTGTGGGATCAAAATGCAAAA 440
DB 361 TTTAACACTAATGGAAGCTTTAAGATACTGTAAGGTTGGTTCTTACTTGAATCTCCAAA 420
QY 441 AT 442
DB 421 AT 422
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RESULT 15

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US-10-488-619-1577
; Sequence 1577, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1577
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; LENGTH: 641
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1577

Query Match      3.5%; Score 33; DB 6; Length 641;
Best Local Similarity 50.3%; Pred. No. 2.8;
Matches 81; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 3 AGAARAGGAAAAAATAGAAAGAGAAAGCGCTTAGTATCTCGGCGACTTGNACCC 62
Db 357 AAACAAAAAAGAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 416

QY 63 AAACCTGAGGATCAAAATTAGGGCACAAGCCCTCTCGGAGAGAGCCATGGGAAGAAAA 122
Db 417 AAAAAAAGAAAAAAGCAAAAAAAGCAAAAAAAGCAAAAAAAGCAAAAAAAGCAAAAAA 476

QY 123 AACTAGAAATCAAGCGAATTGAGAACAAAAAGTAGCCGACAA 163
Db 477 AAAAAAAGCAAAAAAAGCAAAAAAAGCAAAAAAAGCAAAAAAAGCAAAAAAAGCAAAAA 517
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Search completed: May 22, 2006, 07:49:38
Job time : 37 secs